

SEQUENCE LISTING

<110> University of Utah Research Foundation

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Liu, Jin
Prunuske, Amy
Dimaano, Christian

<120> METHODS AND COMPOSITIONS RELATED TO
INHIBITING NUCLEAR ENVELOPE BREAKDOWN

<130> 21101.0045P1

<150> 60/411,248

<151> 2002-09-17

<160> 35

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<211> 1475

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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35     40     45
Asn Ile Val Pro Gly Trp Leu Gln Arg Tyr Phe Asn Lys Asn Glu Asp
50     55     60
Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu
65     70     75     80
Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile
85     90     95
Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu
100    105    110
Pro Ser Thr Thr Ser Thr Ala Ser Asn Tyr Pro Asp Val Leu Thr Arg
115    120    125
Pro Ser Leu His Arg Ser His Leu Asn Phe Ser Met Leu Glu Ser Pro
130    135    140
Ala Leu His Cys Gln Pro Ser Thr Ser Ser Ala Phe Pro Ile Gly Ser
145    150    155    160
Ser Gly Phe Ser Leu Val Lys Glu Ile Lys Asp Ser Thr Ser Gln His
165    170    175
Asp Asp Asp Asn Ile Ser Thr Thr Ser Gly Phe Ser Ser Arg Ala Ser
180    185    190
Asp Lys Asp Ile Thr Val Ser Lys Asn Thr Ser Leu Pro Pro Leu Trp
195    200    205
Ser Pro Glu Ala Glu Arg Ser His Ser Leu Ser Gln His Thr Ala Thr
210    215    220
Ser Ser Lys Lys Pro Ala Phe Asn Leu Ser Ala Phe Gly Thr Leu Ser
225    230    235    240
Pro Ser Leu Gly Asn Ser Ser Ile Leu Lys Thr Ser Gln Leu Gly Asp
245    250    255
Ser Pro Phe Tyr Pro Gly Lys Thr Thr Tyr Gly Gly Ala Ala Ala Ala
260    265    270
Val Arg Gln Ser Lys Leu Arg Asn Thr Pro Tyr Gln Ala Pro Val Arg
275    280    285
Arg Gln Met Lys Ala Lys Gln Leu Ser Ala Gln Ser Tyr Gly Val Thr
290    295    300
Ser Ser Thr Ala Arg Arg Ile Leu Gln Ser Leu Glu Lys Met Ser Ser
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Pro Leu Ala Asp Ala Lys Arg Ile Pro Ser Ile Val Ser Ser Pro Leu
325    330    335

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 Lys Arg Glu Lys Val Asp Ser Gln Tyr Pro Pro Val Gln Arg Leu Met
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 Thr Pro Lys Pro Val Ser Ile Ala Thr Asn Arg Ser Val Tyr Phe Lys
 370 375 380
 Pro Ser Leu Thr Pro Ser Gly Glu Phe Arg Lys Thr Asn Gln Arg Ile
 385 390 395 400
 Asp Asn Lys Cys Ser Thr Gly Tyr Glu Lys Asn Met Thr Pro Gly Gln
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 Asn Arg Glu Gln Arg Glu Ser Gly Phe Ser Tyr Pro Asn Phe Ser Leu
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 Pro Ala Ala Asn Gly Leu Ser Ser Gly Val Gly Gly Gly Gly Lys
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 Met Arg Arg Glu Arg Thr Arg Phe Val Ala Ser Lys Pro Leu Glu Glu
 450 455 460
 Glu Glu Met Glu Val Pro Val Leu Pro Lys Ile Ser Leu Pro Ile Thr
 465 470 475 480
 Ser Ser Ser Leu Pro Thr Phe Asn Phe Ser Ser Pro Glu Ile Thr Thr
 485 490 495
 Ser Ser Pro Ser Pro Ile Asn Ser Ser Gln Ala Leu Thr Asn Lys Val
 500 505 510
 Gln Met Thr Ser Pro Ser Ser Thr Gly Ser Pro Met Phe Lys Phe Ser
 515 520 525
 Ser Pro Ile Val Lys Ser Thr Glu Ala Asn Val Leu Pro Pro Ser Ser
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 Ile Gly Phe Thr Phe Ser Val Pro Val Ala Lys Thr Ala Glu Leu Ser
 545 550 555 560
 Gly Ser Ser Ser Thr Leu Glu Pro Ile Ile Ser Ser Ser Ala His His
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 Val Thr Thr Val Asn Ser Thr Asn Cys Lys Lys Thr Pro Pro Glu Asp
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 Cys Glu Gly Pro Phe Arg Pro Ala Glu Ile Leu Lys Glu Gly Ser Val
 595 600 605
 Leu Asp Ile Leu Lys Ser Pro Gly Phe Ala Ser Pro Lys Ile Asp Ser
 610 615 620
 Val Ala Ala Gln Pro Thr Ala Thr Ser Pro Val Val Tyr Thr Arg Pro
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 Ala Ile Ser Ser Phe Ser Ser Ser Gly Ile Gly Phe Gly Glu Ser Leu
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 Lys Ala Gly Ser Ser Trp Gln Cys Asp Thr Cys Leu Leu Gln Asn Lys
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 Val Thr Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro
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 Arg Asp Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly
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 Lys Thr Thr Leu Ser Ala Ser Gly Thr Gly Phe Gly Asp Lys Phe Lys
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 Pro Val Ile Gly Thr Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys
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 Pro Glu Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr
 740 745 750
 Cys Val Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu
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 Thr Met Thr Ala Ser Ser Ser Ser Cys Thr Val Thr Thr Gly Thr Leu
 770 775 780
 Gly Phe Gly Asp Lys Phe Lys Arg Pro Ile Gly Ser Trp Glu Cys Ser
 785 790 795 800
 Val Cys Cys Val Ser Asn Asn Ala Glu Asp Asn Lys Cys Val Ser Cys
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Met Ser Glu Lys Pro Gly Ser Ser Val Pro Ala Ser Ser Ser Ser Thr
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 Val Pro Val Ser Leu Pro Ser Gly Gly Ser Leu Gly Leu Glu Lys Phe
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 850 855 860
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 Thr Lys Ser Gly Phe Lys Gly Phe Asp Thr Ser Ser Ser Ser Asn
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 930 935 940
 Pro Met Ser Glu Gly Phe Lys Phe Ser Lys Pro Ile Gly Asp Phe Lys
 945 950 955 960
 Phe Gly Val Ser Ser Glu Ser Lys Pro Glu Glu Val Lys Lys Asp Ser
 965 970 975
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 Val Ser Leu Thr Pro Phe Gln Phe Gly Val Ser Asn Leu Gly Gln Glu
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 1345 1350 1355 1360
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<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<210> 4

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4

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 35      40      45
Thr Val Lys Ser Ile Val Pro Gly Trp Leu Gln Lys Tyr Phe Asn Lys
 50      55      60
Gln Glu Glu Glu His Asp Arg Val His Ser Ala Ser Glu Val Ile Val
 65      70      75      80
Asn Asp Thr Glu Ala Arg Glu Asn Asn Ala Gln His His Ile Tyr Asp
 85      90      95
Asp Asp Asp Glu Gly Asn Ser Pro Thr Asp Gly Arg Val Thr Pro
 100      105      110
Glu Pro Val Ile Asn Val Asp Glu Glu Val Pro Ser Thr Ser Gln Ser
 115      120      125
Ala Ile Asn Asn Thr Asp Ala Leu Thr Arg Pro Ser Leu His Arg Ala
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Ser Leu Asn Phe Asn Ile Phe Asp Ser Pro Ala Leu Asn Cys Gln Pro
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Ser Thr Ser Ser Ala Phe Pro Ile Gly Thr Ser Gly Phe Ser Leu Ile
 165      170      175
Lys Glu Ile Lys Asp Ser Thr Ser Gln His Asp Asp Asp Asn Ile Ser
 180      185      190
Thr Thr Ser Gly Phe Thr Ser Arg Ala Ser Asp Lys Asp Leu Ala Val
 195      200      205
Ser Lys Asn Val Ser Val Pro Pro Leu Trp Ser Pro Glu Val Asp Arg
 210      215      220
Ser Gln Ser Leu Ser His Asn Ser Ser Met Thr Ser Lys Lys Pro Thr
 225      230      235      240
Phe Asn Leu Ser Ala Phe Gly Ser Leu Ser Pro Ser Leu Gly Asn Ala
 245      250      255
Ser Ile Leu Asn Arg Gln Leu Gly Asp Ser Pro Phe Tyr Pro Gly Lys
 260      265      270
Thr Thr Tyr Gln Gly Ala Ala Ala Val Arg Ser Ser Arg Val Arg Ala
 275      280      285
Thr Pro Tyr Gln Ala Pro Leu Arg Arg Gln Val Lys Ala Lys Pro Ala
 290      295      300
Ala His Ser Gln Gln Cys Gly Val Thr Ser Ser Ala Ala Arg Arg Ile
 305      310      315      320
Leu Gln Ser Leu Glu Lys Met Ser Ser Pro Leu Ala Asp Ala Lys Arg
 325      330      335
Ile Pro Ser Asn Ser Ser Leu Ser His Thr Pro Glu Lys Asn Val Met
 340      345      350
Asp Ile Pro Glu Asn Pro Ser Lys Arg Lys Lys Val Glu Ser Pro Phe
 355      360      365
Pro Pro Val Gln Arg Leu Val Thr Pro Lys Ser Ile Ser Val Ser Ala
 370      375      380
Asn Arg Ser Leu Tyr Ile Lys Pro Ser Leu Thr Pro Ser Ala Val Ser
 385      390      395      400

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<210> 5

<211> 4305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

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<210> 6

<211> 1219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

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			20				25						30		
Thr	Lys	Asn	Asn	Leu	Gln	Ser	Thr	Ser	Gln	Ser	His	Ser	Phe	Ser	Tyr
		35				40					45				
Pro	Lys	Phe	Ser	Thr	Pro	Ala	Ser	Asn	Gly	Leu	Ser	Ser	Gly	Thr	Gly
	50					55				60					
Gly	Gly	Lys	Met	Met	Arg	Glu	Lys	Gly	Ser	His	Tyr	Ser	Thr	Lys	Pro
65					70					75				80	
Ala	Asn	Glu	Glu	Leu	Asp	Gly	Pro	Val	Leu	Pro	Glu	Ile	Pro	Leu	Pro
			85						90					95	
Leu	Ser	Thr	Ala	Ala	Leu	Pro	Ser	Phe	Gln	Phe	Ser	Thr	Leu	Ser	Gly
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Ser	Ala	Thr	Ser	Pro	Ile	Ser	Val	Thr	Lys	Pro	Ala	Asn	Ser	Thr	Thr
		115					120					125			
Cys	His	Leu	Thr	Ser	Ser	Ser	Pro	Ser	Phe	Thr	Phe	Ser	Ser	Pro	Ile
	130					135						140			
Val	Lys	Ser	Thr	Glu	Ser	Asn	Ala	Gln	Phe	Ser	Gly	Ser	Ser	Val	Asp
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Phe	Thr	Phe	Ser	Val	Pro	Ala	Ala	Lys	Ala	Ser	Ser	Ala	Thr	Ser	Asp
			165						170					175	
Glu	Ser	Lys	Val	Ser	Ala	Val	Ser	Ser	Ala	Ala	Lys	Thr	His	Ala	Ala
			180					185					190		
Val	Asn	Ser	Ser	Ala	Lys	Asn	Thr	Asp	Asp	Glu	Gln	Val	Gly	Phe	Cys
	195					200						205			
Lys	Pro	Ala	Lys	Thr	Leu	Lys	Glu	Gly	Ser	Val	Leu	Asp	Met	Leu	Arg
	210					215						220			
Ser	Pro	Gly	Phe	Ser	Ser	Leu	Pro	Ser	Leu	Leu	Thr	Ser	Glu	Ser	Thr
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Leu	Asn	Arg	Ser	Thr	Pro	Thr	Leu	Ser	Lys	Thr	Val	Gly	Asn	Thr	Phe
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Ser	Pro	Ala	Asn	Val	Ser	Leu	Gly	Val	Gly	Ser	Lys	Gln	Phe	Gly	Leu
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 290 295 300
 Lys Leu Pro Ala Ser Pro Pro Ser Ser Asn Thr Lys Ser Thr Val Pro
 305 310 315 320
 Leu Ser Ser Thr Pro Gly Leu Gly Asp Ile Phe Lys Lys Pro Ala Gly
 325 330 335
 Met Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys Ala Glu Val Thr
 340 345 350
 Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr Cys Ile Lys Ala
 355 360 365
 Thr Leu Leu Ile Pro Ser Thr Thr Lys Ser Ile Asn Pro Ala Thr Asn
 370 375 380
 Thr Leu Ala Phe Ala Ser Cys Ser Ala Ser Ile Pro Asn Glu Glu Met
 385 390 395 400
 Phe Lys Lys Pro Met Gly Ser Trp Glu Cys Thr Val Cys His Met Gln
 405 410 415
 Asn Lys Thr Glu Asp Asn Thr Cys Val Gly Cys Lys Ala Glu Lys Pro
 420 425 430
 Gly Thr Val Lys Ser Val Pro Thr Ala Ala Pro Ser Gly Leu Leu Gly
 435 440 445
 Leu Leu His Gln Phe Lys Lys Pro Thr Gly Ser Trp Asp Cys Asp Val
 450 455 460
 Cys Leu Ile Gln Asn Lys Pro Glu Ala Ala Lys Cys Ile Ala Cys Glu
 465 470 475 480
 Ser Ala Lys Pro Gly Thr Lys Ala Glu Pro Lys Gly Thr Phe Asp Thr
 485 490 495
 Val Lys Asn Ser Val Ser Val Ala Pro Leu Ser Ser Gly Gln Leu Gly
 500 505 510
 Leu Leu Asp Gln Phe Lys Lys Ser Ala Gly Ser Trp Asp Cys Asp Val
 515 520 525
 Cys Leu Val Glu Asn Lys Pro Glu Ala Thr Lys Cys Val Ala Cys Glu
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 Thr Ser Lys Pro Gly Thr Lys Ala Glu Leu Lys Gly Phe Gly Thr Ser
 545 550 555 560
 Thr Phe Ser Ser Gly Thr Ala Ala Pro Thr Phe Lys Phe Gly Val Gln
 565 570 575
 Ser Ser Asp Ser Thr Ala Glu Leu Lys Ser Gly Ala Ser Thr Ser Gly
 580 585 590
 Phe Ala Lys Ser Ile Gly Asp Phe Lys Phe Gly Leu Val Ser Ala Ser
 595 600 605
 Thr Thr Thr Glu Glu Thr Gly Lys Lys Ser Phe Thr Phe Gly Ser Ser
 610 615 620
 Thr Thr Asn Glu Val Ser Ala Gly Phe Lys Phe Gly Ile Ala Gly Ser
 625 630 635 640
 Ala Gln Thr Lys Pro Asp Thr Leu Ser Gln Ser Thr Thr Ser Gly Phe
 645 650 655
 Thr Phe Gly Ser Val Ser Asn Thr Val Ser Leu Ala Pro Ala Ala Thr
 660 665 670
 Ser Ser Ser Ser Thr Gly Leu Gln Val Ala Ala Ala Ile Ala Asp Ser
 675 680 685
 Asn Leu Ala Thr Thr Ala Ala Leu Lys Ser Ala Glu Glu Lys Lys Ala
 690 695 700
 Glu Ala Pro Thr Ile Thr Pro Phe Ser Phe Gly Lys Thr Asp Gln Asn
 705 710 715 720
 Lys Glu Thr Ala Ser Thr Ser Phe Val Phe Gly Lys Lys Asp Glu Lys
 725 730 735
 Thr Asp Ser Ala Pro Thr Gly Ser Ser Phe Ala Phe Gly Leu Lys Lys
 740 745 750

Asp Gly Glu Glu Ser Lys Pro Phe Leu Phe Gly Lys Pro Glu Pro Thr
 755 760 765
 Lys Val Asp Gly Asn Ala Ala Ser Ala Gly Phe Ala Phe Gly Val Thr
 770 775 780
 Asn Pro Thr Glu Lys Lys Asp Ile Glu Gln Pro Gly Lys Ser Val Phe
 785 790 795 800
 Ala Phe Gly Ala Gln Thr Ser Ile Thr Asp Ala Gly Ala Ser Lys Gln
 805 810 815
 Pro Phe Ser Phe Leu Thr Asn Val Ser Ser Thr Ala Ala Ser Ser Ser
 820 825 830
 Thr Cys Gly Val Ser Ser Ser Val Phe Gly Ser Val Thr Gln Ser Ser
 835 840 845
 Thr Pro Ala Thr Pro Ser Asn Val Phe Gly Ser Ala Ile Ser Ala Asn
 850 855 860
 Ala Pro Ala Pro Ser Ser Gly Val Phe Gly Asn Leu Thr Pro Ser Asn
 865 870 875 880
 Ala Pro Ala Ala Ser Ser Thr Leu Phe Gly Asn Val Ala Pro Ser Ser
 885 890 895
 Thr Pro Ser Gly Ser Ser Gly Leu Phe Gly Thr Ala Ala Ala Ser Ser
 900 905 910
 Thr Pro Ala Thr Ser Thr Ser Leu Phe Gly Ser Ala Ala Lys Ser Ser
 915 920 925
 Ala Pro Ala Ser Ser Gly Gly Val Phe Asn Ser Ala Ala Pro Ala Ala
 930 935 940
 Pro Ala Ser Thr Thr Ser Ser Val Phe Gly Ser Val Ala Ser Ser Thr
 945 950 955 960
 Asn Thr Ser Ala Asn Ser Ala Asn Ile Phe Gly Ser Ser Gly Gly Ala
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 Ala Thr Ala Pro Gly Ala Phe Val Phe Gly Gln Pro Ala Ser Thr Ala
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 Ser Thr Val Phe Gly Asn Ser Ser Glu Ser Lys Ser Thr Phe Val Phe
 995 1000 1005
 Ser Gly Gln Glu Asn Lys Pro Val Thr Ser Ala Ser Thr Ser Val Thr
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 Pro Phe Leu Phe Gly Ala Val Ser Ala Thr Thr Pro Ala Ala Pro
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 Ser Ser Pro Phe Ile Phe Gly Ala Gly Ala Ser Gly Ser Ala Ser Ser
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 Ser Ile Thr Ala Gln Ala Asn Pro Val Pro Ala Phe Gly Gln Ser Ser
 1075 1080 1085
 Asn Pro Ser Thr Ala Pro Ala Phe Gly Ser Ser Thr Ser Val Pro Val
 1090 1095 1100
 Phe Pro Ala Gly Ser Ser Gln Gln Val Pro Ala Phe Gly Ser Ser Ser
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 Ala Asn Phe Asn Phe Asn Ser Thr Asn Ser Ser Gly Gly Val Phe Thr
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 Met Phe Asn Ala Ala Ala Pro Gly Phe Asn Ile Gly Thr Asn Gly Arg
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<210> 7
 <211> 10697
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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<211> 3224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

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Ala Lys Leu Tyr Tyr Glu Ala Lys Glu Tyr Asp Leu Ala Lys Lys Tyr
35     40     45
Ile Cys Thr Tyr Ile Asn Val Gln Glu Arg Asp Pro Lys Ala His Arg
50     55     60
Phe Leu Gly Leu Leu Tyr Glu Leu Glu Glu Asn Thr Asp Lys Ala Val
65     70     75     80
Glu Cys Tyr Arg Arg Ser Val Glu Leu Asn Pro Thr Gln Lys Asp Leu
85     90     95
Val Leu Lys Ile Ala Glu Leu Leu Cys Lys Asn Asp Val Thr Asp Gly
100    105    110
Arg Ala Lys Tyr Trp Leu Glu Arg Ala Ala Lys Leu Phe Pro Gly Ser
115    120    125
Pro Ala Ile Tyr Lys Leu Lys Glu Gln Leu Leu Asp Cys Glu Gly Glu
130    135    140
Asp Gly Trp Asn Lys Leu Phe Asp Leu Ile Gln Ser Glu Leu Tyr Val
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Arg Pro Asp Asp Val His Val Asn Ile Arg Leu Val Glu Val Tyr Arg
165    170    175
Ser Thr Lys Arg Leu Lys Asp Ala Val Ala His Cys His Glu Ala Glu
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Arg Asn Ile Ala Leu Arg Ser Ser Leu Glu Trp Asn Ser Cys Val Val
195    200    205
Gln Thr Leu Lys Glu Tyr Leu Glu Ser Leu Gln Cys Leu Glu Ser Asp
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Lys Ser Asp Trp Arg Ala Thr Asn Thr Asp Leu Leu Ala Tyr Ala
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Asn Leu Met Leu Leu Thr Leu Ser Thr Arg Asp Val Gln Glu Ser Arg
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Glu Leu Leu Gln Ser Phe Asp Ser Ala Leu Gln Ser Val Lys Ser Leu
260    265    270
Gly Gly Asn Asp Glu Leu Ser Ala Thr Phe Leu Glu Met Lys Gly His
275    280    285
Phe Tyr Met His Ala Gly Ser Leu Leu Leu Lys Met Gly Gln His Ser
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Ser Asn Val Gln Trp Arg Ala Leu Ser Glu Leu Ala Ala Leu Cys Tyr
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Pro Arg Trp Ala Glu Asp Gln Asn Ser Leu Leu Lys Met Ile Cys Gln
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 Pro Lys Ser Gly Phe Glu Gly Met Phe Thr Lys Lys Glu Gly Gln Trp
 1715 1720 1725
 Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala Ser Ala Thr Lys Cys
 1730 1735 1740
 Ile Ala Cys Gln Cys Pro Ser Lys Gln Asn Gln Thr Thr Ala Ile Ser
 1745 1750 1755 1760

Thr Pro Ala Ser Ser Glu Ile Ser Lys Ala Pro Lys Ser Gly Phe Glu
 1765 1770 1775
 Gly Met Phe Ile Arg Lys Gly Gln Trp Asp Cys Ser Val Cys Cys Val
 1780 1785 1790
 Gln Asn Glu Ser Ser Ser Leu Lys Cys Val Ala Cys Asp Ala Ser Lys
 1795 1800 1805
 Pro Thr His Lys Pro Ile Ala Glu Ala Pro Ser Ala Phe Thr Leu Gly
 1810 1815 1820
 Ser Glu Met Lys Leu His Asp Ser Ser Gly Ser Gln Val Gly Thr Gly
 1825 1830 1835 1840
 Phe Lys Ser Asn Phe Ser Glu Lys Ala Ser Lys Phe Gly Asn Thr Glu
 1845 1850 1855
 Gln Gly Phe Lys Phe Gly His Val Asp Gln Glu Asn Ser Pro Ser Phe
 1860 1865 1870
 Met Phe Gln Gly Ser Ser Asn Thr Glu Phe Lys Ser Thr Lys Glu Gly
 1875 1880 1885
 Phe Ser Ile Pro Val Ser Ala Asp Gly Phe Lys Phe Gly Ile Ser Glu
 1890 1895 1900
 Pro Gly Asn Gln Glu Lys Lys Ser Glu Lys Pro Leu Glu Asn Gly Thr
 1905 1910 1915 1920
 Gly Phe Gln Ala Gln Asp Ile Ser Gly Gln Lys Asn Gly Arg Gly Val
 1925 1930 1935
 Ile Phe Gly Gln Thr Ser Ser Thr Phe Thr Phe Ala Asp Leu Ala Lys
 1940 1945 1950
 Ser Thr Ser Gly Glu Gly Phe Gln Phe Gly Lys Lys Asp Pro Asn Phe
 1955 1960 1965
 Lys Gly Phe Ser Gly Ala Gly Glu Lys Leu Phe Ser Ser Gln Tyr Gly
 1970 1975 1980
 Lys Met Ala Asn Lys Ala Asn Thr Ser Gly Asp Phe Glu Lys Asp Asp
 1985 1990 1995 2000
 Asp Ala Tyr Lys Thr Glu Asp Ser Asp Asp Ile His Phe Glu Pro Val
 2005 2010 2015
 Val Gln Met Pro Glu Lys Val Glu Leu Val Thr Gly Glu Glu Asp Glu
 2020 2025 2030
 Lys Val Leu Tyr Ser Gln Arg Val Lys Leu Phe Arg Phe Asp Ala Glu
 2035 2040 2045
 Val Ser Gln Trp Lys Glu Arg Gly Leu Gly Asn Leu Lys Ile Leu Lys
 2050 2055 2060
 Asn Glu Val Asn Gly Lys Leu Arg Met Leu Met Arg Arg Glu Gln Val
 2065 2070 2075 2080
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 Ser Asp Gly Asp Ala Lys Leu Glu Gln Leu Ala Ala Lys Phe Lys Thr
 2115 2120 2125
 Pro Glu Leu Ala Glu Glu Phe Lys Gln Lys Phe Glu Glu Cys Gln Arg
 2130 2135 2140
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 Gly Arg Ala Ala Lys Leu Ile Gln Arg Ala Glu Glu Met Lys Ser Gly
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 Leu Lys Asp Phe Lys Thr Phe Leu Thr Asn Asp Gln Thr Lys Val Thr
 2180 2185 2190
 Glu Glu Glu Asn Lys Gly Ser Gly Thr Gly Ala Ala Gly Ala Ser Asp
 2195 2200 2205
 Thr Thr Ile Lys Pro Asn Pro Glu Asn Thr Gly Pro Thr Leu Glu Trp
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 2225 2230 2235 2240

Ser Ser Val His Ala Ser Pro Leu Ala Ser Ser Pro Val Arg Lys Asn
 2245 2250 2255
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 2305 2310 2315 2320
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 2325 2330 2335
 Ala Lys Leu Tyr Arg Tyr Asp Lys Asp Val Gly Gln Trp Lys Glu Arg
 2340 2345 2350
 Gly Ile Gly Asp Ile Lys Ile Leu Gln Asn Tyr Asp Asn Lys Gln Val
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 2370 2375 2380
 Arg Ile Thr Pro Asp Met Thr Leu Gln Asn Met Lys Gly Thr Glu Arg
 2385 2390 2395 2400
 Val Trp Leu Trp Thr Ala Cys Asp Phe Ala Asp Gly Glu Arg Lys Val
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 Glu His Leu Ala Val Arg Phe Lys Leu Gln Asp Val Ala Asp Ser Phe
 2420 2425 2430
 Lys Lys Ile Phe Asp Glu Ala Lys Thr Ala Gln Glu Lys Asp Ser Leu
 2435 2440 2445
 Ile Thr Pro His Val Ser Arg Ser Ser Thr Pro Arg Glu Ser Pro Cys
 2450 2455 2460
 Gly Lys Ile Ala Val Ala Val Leu Glu Glu Thr Thr Arg Glu Arg Thr
 2465 2470 2475 2480
 Asp Val Ile Gln Gly Asp Asp Val Ala Asp Ala Thr Ser Glu Val Glu
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 Val Ser Ser Thr Ser Glu Thr Thr Pro Lys Ala Val Val Ser Pro Pro
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 Lys Ser Lys Pro Phe Ala Phe Gly Asn Ser Ser Ala Thr Gly Ser Leu
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 Phe Gly Phe Ser Phe Asn Ala Pro Leu Lys Ser Asn Asn Ser Glu Thr
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 Ser Ser Val Ala Gln Ser Gly Ser Glu Ser Lys Val Glu Pro Lys Lys
 2565 2570 2575
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 Val Lys Asn Leu Phe Ala Ser Phe Pro Thr Glu Glu Ser Ser Ile Asn
 2595 2600 2605
 Tyr Thr Phe Lys Thr Pro Glu Lys Ala Lys Glu Lys Lys Lys Pro Glu
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 Asp Ser Pro Ser Asp Asp Val Leu Ile Val Tyr Glu Leu Thr Pro
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 Thr Ala Glu Gln Lys Ala Leu Ala Thr Lys Leu Lys Leu Pro Pro Thr
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 2660 2665 2670
 Asp Asp Glu Asp Phe Glu Thr Ala Val Lys Lys Leu Asn Gly Lys Leu
 2675 2680 2685
 Tyr Leu Asp Gly Ser Glu Lys Cys Arg Pro Leu Glu Glu Asn Thr Ala
 2690 2695 2700
 Asp Asn Glu Lys Glu Cys Ile Ile Val Trp Glu Lys Lys Pro Thr Val
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Glu Glu Lys Ala Lys Ala Asp Thr Leu Lys Leu Pro Pro Thr Phe Phe
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 Cys Gly Val Cys Ser Asp Thr Asp Glu Asp Asn Gly Asn Gly Glu Asp
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 Lys His Val Val Phe Gly Phe Val Lys Asp Gly Met Asp Thr Val Lys
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 <213> Artificial Sequence

<220>
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<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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          35          40          45
Asn Arg Asn Lys Thr Gly Glu Ile Thr Ala Ser Ser Asn Lys Ser Leu
          50          55          60
Asn Leu Leu Lys Ile Lys His Gly Asp Leu Leu Phe Leu Phe Pro Ser
          65          70          75          80
Ser Leu Ala Gly Pro Ser Ser Glu Met Glu Thr Ser Val Pro Pro Gly
          85          90          95
Phe Lys Val Phe Gly Ala Pro Asn Val Val Glu Asp Glu Ile Asp Gln
          100          105          110
Tyr Leu Ser Lys Gln Asp Gly Lys Ile Tyr Arg Ser Arg Asp Pro Gln
          115          120          125
Leu Cys Arg His Gly Pro Leu Gly Lys Cys Val His Cys Val Pro Leu
          130          135          140
Glu Pro Phe Asp Glu Asp Tyr Leu Asn His Leu Glu Pro Pro Val Lys
          145          150          155          160
His Met Ser Phe His Ala Tyr Ile Arg Lys Leu Thr Gly Gly Ala Asp
          165          170          175

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Lys Gly Lys Phe Val Ala Leu Glu Asn Ile Ser Cys Lys Ile Lys Ser
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 Gly Cys Glu Gly His Leu Pro Trp Pro Asn Gly Ile Cys Thr Lys Cys
 195 200 205
 Gln Pro Ser Ala Ile Thr Leu Asn Arg Gln Lys Tyr Arg His Val Asp
 210 215 220
 Asn Ile Met Phe Glu Asn His Thr Val Ala Asp Arg Phe Leu Asp Phe
 225 230 235 240
 Trp Arg Lys Thr Gly Asn Gln Gln Phe Gly Tyr Leu Tyr Gly Arg Tyr
 245 250 255
 Thr Glu His Lys Asp Ile Pro Leu Gly Ile Arg Ala Glu Val Ala Ala
 260 265 270
 Ile Tyr Glu Pro Pro Gln Ile Gly Thr Gln Asn Ser Leu Glu Leu Leu
 275 280 285
 Glu Asp Pro Lys Ala Glu Val Val Asp Glu Ile Ala Ala Lys Leu Gly
 290 295 300
 Leu Arg Lys Val Gly Trp Ile Phe Thr Asp Leu Val Ser Glu Asp Thr
 305 310 315 320
 Arg Lys Gly Thr Val Arg Tyr Ser Arg Asn Lys Asp Thr Tyr Phe Leu
 325 330 335
 Ser Ser Glu Glu Cys Ile Thr Ala Gly Asp Phe Gln Asn Lys His Pro
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 Tyr Gln Val Ser Asn Gln Cys Met Ala Leu Val Arg Asp Glu Cys Leu
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 405 410 415
 Ser Glu Gln Tyr Val Pro Asp Val Phe Tyr Lys Asp Val Asp Lys Phe
 420 425 430
 Gly Asn Glu Ile Thr Gln Leu Ala Arg Pro Leu Pro Val Glu Tyr Leu
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 Ile Ile Asp Ile Thr Thr Thr Phe Pro Lys Asp Pro Val Tyr Thr Phe
 450 455 460
 Ser Ile Ser Gln Asn Pro Phe Pro Ile Glu Asn Arg Asp Val Leu Gly
 465 470 475 480
 Glu Thr Gln Asp Phe His Ser Leu Ala Thr Tyr Leu Ser Gln Asn Thr
 485 490 495
 Ser Ser Val Phe Leu Asp Thr Ile Ser Asp Phe His Leu Leu Leu Phe
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 Leu Val Thr Asn Glu Val Met Pro Leu Gln Asp Ser Ile Ser Leu Leu
 515 520 525
 Leu Glu Ala Val Arg Thr Arg Asn Glu Glu Leu Ala Gln Thr Trp Lys
 530 535 540
 Arg Ser Glu Gln Trp Ala Thr Ile Glu Gln Leu Cys Ser Thr Val Gly
 545 550 555 560
 Gly Gln Leu Pro Gly Leu His Glu Tyr Gly Ala Val Glu Gly Ser Thr
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<211> 3067

<212> DNA

<213> Artificial Sequence

<220>

synthetic construct

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tccctggatt aaaagaagcc tttgttgtt gaaagtgggt gaaggaaaac catgctgac 2520
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tcgaactaga agtagatttg gataatttgg aattagaaga tattgacaca acagatatca 2760
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gatcattatt atatataggt attgattgct accctgacca cagtgccttg gactatgaga 2880
aacttcttag atttttatat gtaaagtctg tggaccactg ggagcacaat gccacatca 2940
tcttaagaag agtttatgtg cagcatttaa atcactgtgt tttccttgtt aactaaaaca 3000
gacatgggct ttgatttttt tcatactatt agaccatatt tcataaaacc ttttgaatta 3060
aaaaaaa
3067

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<210> 12

<211> 906

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

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Met Pro Leu Arg Leu Asp Ile Lys Arg Lys Leu Thr Ala Arg Ser Asp
 1          5          10          15
Arg Val Lys Ser Val Asp Leu His Pro Thr Glu Pro Trp Met Leu Ala
      20          25          30
Ser Leu Tyr Asn Gly Ser Val Cys Val Trp Asn His Glu Thr Gln Thr
      35          40          45
Leu Val Lys Thr Phe Glu Val Cys Asp Leu Pro Val Arg Ala Ala Lys
      50          55          60
Phe Val Ala Arg Lys Asn Trp Val Val Thr Gly Ala Asp Asp Met Gln
      65          70          75          80
Ile Arg Val Phe Asn Tyr Asn Thr Leu Glu Arg Val His Met Phe Glu
      85          90          95
Ala His Ser Asp Tyr Ile Arg Cys Ile Ala Val His Pro Thr Gln Pro
      100          105          110
Phe Ile Leu Thr Ser Ser Asp Asp Met Leu Ile Lys Leu Trp Asp Trp
      115          120          125
Asp Lys Lys Trp Ser Cys Ser Gln Val Phe Glu Gly His Thr His Tyr
      130          135          140
Val Met Gln Ile Val Ile Asn Pro Lys Asp Asn Asn Gln Phe Ala Ser
      145          150          155          160
Ala Ser Leu Asp Arg Thr Ile Lys Val Trp Gln Leu Gly Ser Ser Ser
      165          170          175
Pro Asn Phe Thr Leu Glu Gly His Glu Lys Gly Val Asn Cys Ile Asp
      180          185          190
Tyr Tyr Ser Gly Gly Asp Lys Pro Tyr Leu Ile Ser Gly Ala Asp Asp
      195          200          205
Arg Leu Val Lys Ile Trp Asp Tyr Gln Asn Lys Thr Cys Val Gln Thr
      210          215          220
Leu Glu Gly His Ala Gln Asn Val Ser Cys Ala Ser Phe His Pro Glu
      225          230          235          240
Leu Pro Ile Ile Ile Thr Gly Ser Glu Asp Gly Thr Val Arg Ile Trp
      245          250          255
His Ser Ser Thr Tyr Arg Leu Glu Ser Thr Leu Asn Tyr Gly Met Glu
      260          265          270
Arg Val Trp Cys Val Ala Ser Leu Arg Gly Ser Asn Asn Val Ala Leu
      275          280          285
Gly Tyr Asp Glu Gly Ser Ile Ile Val Lys Leu Gly Arg Glu Glu Pro
      290          295          300
Ala Met Ser Met Asp Ala Asn Gly Lys Ile Ile Trp Ala Lys His Ser
      305          310          315          320
Glu Val Gln Gln Ala Asn Leu Lys Ala Met Gly Asp Ala Glu Ile Lys
      325          330          335
Asp Gly Glu Arg Leu Pro Leu Ala Val Lys Asp Met Gly Ser Cys Glu
      340          345          350
Ile Tyr Pro Gln Thr Ile Gln His Asn Pro Asn Gly Arg Phe Val Val
      355          360          365
Val Cys Gly Asp Gly Glu Tyr Ile Ile Tyr Thr Ala Met Ala Leu Arg
      370          375          380
Asn Lys Ser Phe Gly Ser Ala Gln Glu Phe Ala Trp Ala His Asp Ser
      385          390          395          400
Ser Glu Tyr Ala Ile Arg Glu Ser Asn Ser Ile Val Lys Ile Phe Lys
      405          410          415
Asn Phe Lys Glu Lys Lys Ser Phe Lys Pro Asp Phe Gly Ala Glu Ser
      420          425          430
Ile Tyr Gly Gly Phe Leu Leu Gly Val Arg Ser Val Asn Gly Leu Ala
      435          440          445

```

Phe Tyr Asp Trp Asp Asn Thr Glu Leu Ile Arg Arg Ile Glu Ile Gln
 450 455 460
 Pro Lys His Ile Phe Trp Ser Asp Ser Gly Glu Leu Val Cys Ile Ala
 465 470 475 480
 Thr Glu Glu Ser Phe Phe Ile Leu Lys Tyr Leu Ser Glu Lys Val Leu
 485 490 495
 Ala Ala Gln Glu Thr His Glu Gly Val Thr Glu Asp Gly Ile Glu Asp
 500 505 510
 Ala Phe Glu Val Leu Gly Glu Ile Gln Glu Ile Val Lys Thr Gly Leu
 515 520 525
 Trp Val Gly Asp Cys Phe Ile Tyr Thr Ser Ser Val Asn Arg Leu Asn
 530 535 540
 Tyr Tyr Val Gly Gly Glu Ile Val Thr Ile Ala His Leu Asp Arg Thr
 545 550 555 560
 Met Tyr Leu Leu Gly Tyr Ile Pro Lys Asp Asn Arg Leu Tyr Leu Gly
 565 570 575
 Asp Lys Glu Leu Asn Ile Ile Ser Tyr Ser Leu Leu Val Ser Val Leu
 580 585 590
 Glu Tyr Gln Thr Ala Val Met Arg Arg Asp Phe Ser Met Ala Asp Lys
 595 600 605
 Val Leu Pro Thr Ile Pro Lys Glu Gln Arg Thr Arg Val Ala His Phe
 610 615 620
 Leu Glu Lys Gln Gly Phe Lys Gln Gln Ala Leu Thr Val Ser Thr Asp
 625 630 635 640
 Pro Glu His Arg Phe Glu Leu Ala Leu Gln Leu Gly Glu Leu Lys Ile
 645 650 655
 Ala Tyr Gln Leu Ala Val Glu Ala Glu Ser Glu Gln Lys Trp Lys Gln
 660 665 670
 Leu Ala Glu Leu Ala Ile Ser Lys Cys Gln Phe Gly Leu Ala Gln Glu
 675 680 685
 Cys Leu His His Ala Gln Asp Tyr Gly Gly Leu Leu Leu Ala Thr
 690 695 700
 Ala Ser Gly Asn Ala Asn Met Val Asn Lys Leu Ala Glu Gly Ala Glu
 705 710 715 720
 Arg Asp Gly Lys Asn Asn Val Ala Phe Met Ser Tyr Phe Leu Gln Gly
 725 730 735
 Lys Val Asp Ala Cys Leu Glu Leu Leu Ile Arg Thr Gly Arg Leu Pro
 740 745 750
 Glu Ala Ala Phe Leu Ala Arg Thr Tyr Leu Pro Ser Gln Val Ser Arg
 755 760 765
 Val Val Lys Leu Trp Arg Glu Asn Leu Ser Lys Val Asn Gln Lys Ala
 770 775 780
 Ala Glu Ser Leu Ala Asp Pro Thr Glu Tyr Glu Asn Leu Phe Pro Gly
 785 790 795 800
 Leu Lys Glu Ala Phe Val Val Glu Glu Trp Val Lys Glu Thr His Ala
 805 810 815
 Asp Leu Trp Pro Ala Lys Gln Tyr Pro Leu Val Thr Pro Asn Glu Glu
 820 825 830
 Arg Asn Val Met Glu Glu Gly Lys Asp Phe Gln Pro Ser Arg Ser Thr
 835 840 845
 Ala Gln Gln Glu Leu Asp Gly Lys Pro Ala Ser Pro Thr Pro Val Ile
 850 855 860
 Val Ala Ser His Thr Ala Asn Lys Glu Glu Lys Ser Leu Leu Glu Leu
 865 870 875 880
 Glu Val Asp Leu Asp Asn Leu Glu Leu Glu Asp Ile Asp Thr Thr Asp
 885 890 895
 Ile Asn Leu Asp Glu Asp Ile Leu Asp Asp
 900 905

<210> 13

<211> 914

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

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ggcggcgagc ggaatgcagc ggcccagaggc ctggccacgt ccgcacccgg gggagggggc      60
cgcgcgggcc caggccgggg gcccgggccgc gcctgctcga gccgggggagc cctcggggct      120
gcggttgacg gaaccttccc tctacacccat caaggctgtt ttcatoctag ataatgacgg      180
gcgcccggctg ctggccaagt attatgatga cacattcccc tccatgaagg agcagatggt      240
tttcgagaaa aatgtcttca acaagaccag ccggactgag agtgagattg cattttttgg      300
gggtatgacc atcgtctaca agaacagcat tgacctcttc ctatacgtgg tgggctcatc      360
ctacgagaat gagctgatgc tcatgtctgt tctcacctgc ctgtttgagt ctctgaacca      420
catgttaagg aagaacgtgg agaagcgctg gttgctggag aacatggacg gagccttctt      480
ggtgctggac gagattgtgg atggcggtgt gattctggag agtgaccccc agcaagtgat      540
ccagaagggtg aattttaggg cagatgatgg cggcttgact gaacagagtg tggcccaggt      600
tcttcagttc gccaaaggaa aaattaaatg gtcgttattg aaatgaaggc tgtggattca      660
aggctccctg ccccccagac catttcccca atcctggcaa aagcccaaag atcccagggt      720
caggagagac ccctctgtat ccccaggctc ctcccagaa tgactcctaa ggtctccagc      780
cagggtctct gagatgcaaa ggtttggcct caggagagtc accttttctc acggccctgg      840
ccttaactca tatcttaggc attcctggcc ccagggccct aataaacctg cttttgtctt      900
ctgcaaaaaa aaaa

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<210> 14

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

```

Met Gln Arg Pro Glu Ala Trp Pro Arg Pro His Pro Gly Glu Gly Ala
1      5      10      15
Ala Ala Ala Gln Ala Gly Gly Pro Ala Pro Pro Ala Arg Ala Gly Glu
20      25      30
Pro Ser Gly Leu Arg Leu Gln Glu Pro Ser Leu Tyr Thr Ile Lys Ala
35      40      45
Val Phe Ile Leu Asp Asn Asp Gly Arg Arg Leu Leu Ala Lys Tyr Tyr
50      55      60
Asp Asp Thr Phe Pro Ser Met Lys Glu Gln Met Val Phe Glu Lys Asn
65      70      75      80
Val Phe Asn Lys Thr Ser Arg Thr Glu Ser Glu Ile Ala Phe Phe Gly
85      90      95
Gly Met Thr Ile Val Tyr Lys Asn Ser Ile Asp Leu Phe Leu Tyr Val
100      105      110
Val Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ser Val Leu Thr
115      120      125
Cys Leu Phe Glu Ser Leu Asn His Met Leu Arg Lys Asn Val Glu Lys
130      135      140
Arg Trp Leu Leu Glu Asn Met Asp Gly Ala Phe Leu Val Leu Asp Glu
145      150      155      160
Ile Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Ile
165      170      175
Gln Lys Val Asn Phe Arg Ala Asp Asp Gly Gly Leu Thr Glu Gln Ser
180      185      190
Val Ala Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu
195      200      205

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Leu Lys
210

<210> 15

<211> 5064

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15

gagaagggga	ccttcaggtc	caggcaaagg	gggaacttct	gtcgtgggaa	cgaaaaagaa	60
agaggattta	cagggtgggg	ggacagaggg	gcagcaggaa	ccagaaggga	gacagtggcg	120
gtcgccaccg	ggccgatccg	agagttcccc	ttagagaacg	gagctcacgg	gcggggaggc	180
ctcacctgct	agtaggacgc	agaaagacag	aaggcgaagg	agacccctg	ccgtagccat	240
cttgccctct	tgctgagcgg	aagcccccg	tcggctcctg	tctgttagcg	gcctctctag	300
gctaccactg	acacgcgtct	tgtggcccg	agcctaagag	accggaagtt	cgtgtttcca	360
ggcgcttccg	gaaaccgcgg	gagagggtcg	ctgacgtgga	ggcgccgaa	gggcagcagg	420
gtgtgtcggg	gctcggatta	agacatcgga	gtcggagacc	tgagagatgt	taaccaaatt	480
cgagaccaag	agcgcgcggg	tcaaagggt	cagctttcac	cccaaagac	cttgatccct	540
gactagttaa	cataatgggg	tcatccagtt	atgggactat	cggatgtgca	ctctcattga	600
caagtttgat	gaacatgatg	gtccagtgcg	agggcattgac	ttccataagc	agcagccact	660
gttcgtctct	ggaggagatg	actataagat	taagggttgg	aattacaagc	ttcggcgctg	720
tcttttcaca	ttgcttgggc	acttagatta	tattcgacac	acgttttttc	atcatgaata	780
tcctctggatt	ctgagtgctt	ccgatgatca	gaccatccga	gtgtggaatt	ggcaatctag	840
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cacagaagac	ttggtagtat	cagccagcct	ggaccagact	gtgcgcgttt	gggatatttc	960
tgggtctgagg	aaaaaaaacc	tgtcccctgg	tgcggtggaa	tcggatgtga	gaggaataac	1020
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ctatgctggt	catggcaata	tgctacacta	tgtcaaggac	cgattcttac	gacagctgga	1500
tttcaacagc	tccaaagatg	tagctgtgat	gcagttgcgg	agtgggtcca	agtttccagt	1560
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ccaacatggc	aacaccccg	ctctaataaa	aataataaaa	ttagcctggc	atggtagcat	4560
gcgcctatag	tcccagctgc	tcaggaggct	gaggcatgag	aatcgcttga	acctaggagg	4620
tggagggtgc	attcaactga	gatcatacca	cttcattcca	gcctgggtga	cagagcaaga	4680
ctctgtctca	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaggaaaac	tctgtgatgg	4740
acatttggtt	agtaaatecc	ttcagtattt	atccctcctt	tccccacagc	agctttcttt	4800
cctgtcaact	agaaaggagc	aggatgtaat	aaatacatct	tgggtgtgact	aggccacacc	4860
aactcttaat	catctcccat	tttctttaga	cattttaaatt	tcaaggcagg	tacctctgt	4920
gtactcagaa	atttgaagaa	gttatttggt	tttccaaaat	gcacactgcg	ggttattgat	4980
ttgttcttta	caactattgt	tctcatattt	ctcacactaa	ataaatctct	atgagagctt	5040
cttgaaaaaa	aaaaaaaaaa	agcg				5064

<210> 16

<211> 1224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

Met	Leu	Thr	Lys	Phe	Glu	Thr	Lys	Ser	Ala	Arg	Val	Lys	Gly	Leu	Ser
1				5					10					15	
Phe	His	Pro	Lys	Arg	Pro	Trp	Ile	Leu	Thr	Ser	Leu	His	Asn	Gly	Val
			20				25						30		
Ile	Gln	Leu	Trp	Asp	Tyr	Arg	Met	Cys	Thr	Leu	Ile	Asp	Lys	Phe	Asp
		35				40						45			
Glu	His	Asp	Gly	Pro	Val	Arg	Gly	Ile	Asp	Phe	His	Lys	Gln	Gln	Pro
	50					55				60					
Leu	Phe	Val	Ser	Gly	Gly	Asp	Asp	Tyr	Lys	Ile	Lys	Val	Trp	Asn	Tyr
65					70					75					80

Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile
 85 90 95
 Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser
 100 105 110
 Asp Asp Gln Thr Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val
 115 120 125
 Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His
 130 135 140
 Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg
 145 150 155 160
 Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala
 165 170 175
 Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr
 180 185 190
 Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val
 195 200 205
 Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala
 210 215 220
 Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp
 225 230 235 240
 Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val
 245 250 255
 Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser
 260 265 270
 Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg
 275 280 285
 Arg Asp His Asp Arg Phe Trp Val Leu Ala Ala His Pro Asn Leu Asn
 290 295 300
 Leu Phe Ala Ala Gly His Asp Gly Gly Met Ile Val Phe Lys Leu Glu
 305 310 315 320
 Arg Glu Arg Pro Ala Tyr Ala Val His Gly Asn Met Leu His Tyr Val
 325 330 335
 Lys Asp Arg Phe Leu Arg Gln Leu Asp Phe Asn Ser Ser Lys Asp Val
 340 345 350
 Ala Val Met Gln Leu Arg Ser Gly Ser Lys Phe Pro Val Phe Asn Met
 355 360 365
 Ser Tyr Asn Pro Ala Glu Asn Ala Val Leu Leu Cys Thr Arg Ala Ser
 370 375 380
 Asn Leu Glu Asn Ser Thr Tyr Asp Leu Tyr Thr Ile Pro Lys Asp Ala
 385 390 395 400
 Asp Ser Gln Asn Pro Asp Ala Pro Glu Gly Lys Arg Ser Ser Gly Leu
 405 410 415
 Thr Ala Val Trp Val Ala Arg Asn Arg Phe Ala Val Leu Asp Arg Met
 420 425 430
 His Ser Leu Leu Ile Lys Asn Leu Lys Asn Glu Ile Thr Lys Lys Val
 435 440 445
 Gln Val Pro Asn Cys Asp Glu Ile Phe Tyr Ala Gly Thr Gly Asn Leu
 450 455 460
 Leu Leu Arg Asp Ala Asp Ser Ile Thr Leu Phe Asp Val Gln Gln Lys
 465 470 475 480
 Arg Thr Leu Ala Ser Val Lys Ile Ser Lys Val Lys Tyr Val Ile Trp
 485 490 495
 Ser Ala Asp Met Ser His Val Ala Leu Ala Lys His Ala Ile Val
 500 505 510
 Ile Cys Asn Arg Lys Leu Asp Ala Leu Cys Asn Ile His Glu Asn Ile
 515 520 525
 Arg Val Lys Ser Gly Ala Trp Asp Glu Ser Gly Val Phe Ile Tyr Thr
 530 535 540
 Thr Ser Asn His Ile Lys Tyr Ala Val Thr Thr Gly Asp His Gly Ile
 545 550 555 560

Ile Arg Thr Leu Asp Leu Pro Ile Tyr Val Thr Arg Val Lys Gly Asn
 565 570 575
 Asn Val Tyr Cys Leu Asp Arg Glu Cys Arg Pro Arg Val Leu Thr Ile
 580 585 590
 Asp Pro Thr Glu Phe Lys Phe Lys Leu Ala Leu Ile Asn Arg Lys Tyr
 595 600 605
 Asp Glu Val Leu His Met Val Arg Asn Ala Lys Leu Val Gly Gln Ser
 610 615 620
 Ile Ile Ala Tyr Leu Gln Lys Lys Gly Tyr Pro Glu Val Ala Leu His
 625 630 635 640
 Phe Val Lys Asp Glu Lys Thr Arg Phe Ser Leu Ala Leu Glu Cys Gly
 645 650 655
 Asn Ile Glu Ile Ala Leu Glu Ala Ala Lys Ala Leu Asp Asp Lys Asn
 660 665 670
 Cys Trp Glu Lys Leu Gly Glu Val Ala Leu Leu Gln Gly Asn His Gln
 675 680 685
 Ile Val Glu Met Cys Tyr Gln Arg Thr Lys Asn Phe Asp Lys Val Ser
 690 695 700
 Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys Leu Arg Lys Met Met
 705 710 715 720
 Lys Ile Ala Glu Ile Arg Lys Asp Met Ser Gly His Tyr Gln Asn Ala
 725 730 735
 Leu Tyr Leu Gly Asp Val Ser Glu Arg Val Arg Ile Leu Lys Asn Cys
 740 745 750
 Gly Gln Lys Ser Leu Ala Tyr Leu Thr Ala Ala Thr His Gly Leu Asp
 755 760 765
 Glu Glu Ala Glu Ser Leu Lys Glu Thr Phe Asp Pro Glu Lys Glu Thr
 770 775 780
 Ile Pro Asp Ile Asp Pro Asn Ala Lys Leu Leu Gln Pro Pro Ala Pro
 785 790 795 800
 Ile Met Pro Leu Asp Thr Asn Trp Pro Leu Leu Thr Val Ser Lys Gly
 805 810 815
 Phe Phe Glu Gly Thr Ile Ala Ser Lys Gly Lys Gly Gly Ala Leu Ala
 820 825 830
 Ala Asp Ile Asp Ile Asp Thr Val Gly Thr Glu Gly Trp Gly Glu Asp
 835 840 845
 Ala Glu Leu Gln Leu Asp Glu Asp Gly Phe Val Glu Ala Thr Glu Gly
 850 855 860
 Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Gly Gly Gly Trp
 865 870 875 880
 Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro
 885 890 895
 Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys
 900 905 910
 Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val
 915 920 925
 Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His
 930 935 940
 Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu
 945 950 955 960
 Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu
 965 970 975
 Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu
 980 985 990
 Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln
 995 1000 1005
 Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu Glu
 1010 1015 1020
 Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu Leu Val
 1025 1030 1035 1040

Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu Ile Thr Ile
1045 1050 1055
Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr Glu Arg Lys Lys
1060 1065 1070
Leu Pro Lys Glu Thr Leu Glu Gln Gln Lys Arg Ile Cys Glu Met Ala
1075 1080 1085
Ala Tyr Phe Thr His Ser Asn Leu Gln Pro Val His Met Ile Leu Val
1090 1095 1100
Leu Arg Thr Ala Leu Asn Leu Phe Phe Lys Leu Lys Asn Phe Lys Thr
1105 1110 1115 1120
Ala Ala Thr Phe Ala Arg Arg Leu Leu Glu Leu Gly Pro Lys Pro Glu
1125 1130 1135
Val Ala Gln Gln Thr Arg Lys Ile Leu Ser Ala Cys Glu Lys Asn Pro
1140 1145 1150
Thr Asp Ala Tyr Gln Leu Asn Tyr Asp Met His Asn Pro Phe Asp Ile
1155 1160 1165
Cys Ala Ala Ser Tyr Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys
1170 1175 1180
Cys Pro Leu Ser Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile
1185 1190 1195 1200
Cys Arg Val Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu
1205 1210 1215
Arg Ile Ser Pro Leu Gln Phe Arg
1220

<210> 17

<211> 1208

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

ctgggtgagaa	gacagcgaaa	tggcgccctcc	ggcccccggc	cgggcctccg	gcggtccgg	60
ggaggtagac	gagctgttcg	acgtaaagaa	cgcccttctac	atcggcagct	accagcagtg	120
cataaacgag	gcgcagcggg	tgaagctgtc	aagcccagag	agagacgtgg	agagggacgt	180
cttctgtat	agagcgtacc	tggcgccagag	gaagttcggg	gtggctcctgg	atgagatcaa	240
gccctcctcg	gccccctgagc	tccagggcgt	gcgcattgtt	gctgactacc	tcgcccacga	300
gagtcggagg	gacagcatcg	tggccgagct	ggaccgagag	atgagcagga	gcgtggacgt	360
gaccaacacc	accttcctgc	tcatggccgc	ctccatctat	ctccacgacc	agaacccgga	420
tggccgacctg	cgtgcgctgc	accaggggga	cagcctggag	tgcacagcca	tgacagtgca	480
gatcctgctg	aagctggacc	gcctggacct	cgcccgaag	gagctgaaga	gaatgcagga	540
cctggacgag	gatgccaccc	tcacccagct	cgccactgcc	tgggtcagcc	tggccacggg	600
tggtgagaag	ctgcaggatg	cctactacat	cttcaggag	atggctgaca	agtgtctgcc	660
caccctgctg	ctgctcaatg	ggcaggcggc	ctgccacatg	gccaggggcc	gctgggaggc	720
cgctgagggc	ctgctgcagg	aggcgctaga	caaggatagt	ggctacccgg	agacgtgggt	780
caacctcatc	gtcctgtccc	agcacctggg	caagccccct	gaggtgacaa	accgatacct	840
gtcccagctg	aaggatgccc	acaggtccca	tcccttcac	aaggagtacc	aggccaagga	900
gaacgacttt	gacaggctgg	tgctacagta	cgctcccagc	gcctgaggct	ggcccagagc	960
tgtcaggacc	atgaagccag	gacagaggcc	aggagccagc	cctgcagccc	tcccaccccg	1020
gcattccacct	gcattccctc	tggggggcagg	agcccacccc	cagcaccccc	atctgttaat	1080
aaatatctca	actccagggt	gttccacctg	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1140
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa						1208

<210> 18

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

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Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
 1           5           10           15
Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
 20           25           30
Gln Cys Ile Asn Glu Ala Gln Arg Val Lys Leu Ser Ser Pro Glu Arg
 35           40           45
Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
 50           55           60
Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
 65           70           75           80
Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
 85           90           95
Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Val
100           105           110
Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu
115           120           125
His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp
130           135           140
Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp
145           150           155           160
Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp
165           170           175
Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala
180           185           190
Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met
195           200           205
Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala
210           215           220
Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln
225           230           235           240
Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu
245           250           255
Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg
260           265           270
Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys
275           280           285
Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr
290           295           300
Ala Pro Ser Ala
305

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<210> 19

<211> 3528

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 19

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agccaaggac tctggagccg ccgcccgcgc tgctgcgggt catatccgga gtagacggag      60
ccgcagtaga cggatccgcg gctgcaccaa accactgccc ctccgagcct gtagtggggc      120
cacaagcccc cagtcccaga ggcgtggtgg gtcgggcaga gtcggaagaa ctggctttct      180
agctggaaga tgcggaaggg gagcgactag gccgcttgcg tctgggcctg gcagaaggga      240

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cgggattttc	tggtcatcctt	aaatccttgtg	tcaaggattg	gttataatat	aaccagaaac	300
catgacggcg	gctgagaacg	tatgctacac	gttaattaac	gtgccaatgg	attcagaacc	360
accatctgaa	attagcttaa	aaaatgatct	agaaaaagga	gatgtaaagt	caaagactga	420
agctttgaa	aaagtaatca	ttatgattct	gaatgggtgaa	aaacttcctg	gacttctgat	480
gaccatcatt	cgttttgtgc	tacctcttca	ggatcacact	atcaagaaat	tacttctggg	540
atthtgggaa	attgttccta	aaacaactcc	agatgggaga	cttttacatg	agatgatcct	600
tgtatgtgat	gcatacagaa	aggatcttca	acatccta	gaatttat	gaggatctac	660
tcttcggttt	ctttgcaaat	tgaaagaagc	agaattgcta	gaacctttaa	tgccagctat	720
tcgtgcatgt	ttggagcatc	gacacagcta	tgtagaaga	aatgctgttt	tgccatcta	780
taccatctat	agaaattttg	aacatcttat	acctgatgct	cctgaactga	tacatgattt	840
tctgggtgaat	gagaaggatg	caagtgtgaa	aaggaatgca	tttatgatgc	taattcatgc	900
agatcaggat	cgagctttgg	attacttaag	tacttgcat	gatcaagttc	aaacatttgg	960
agacattctg	cagctgggtta	ttgttgaact	gatttataag	gtctgtcatg	ctaattccatc	1020
agaaagagct	cgttttat	gctgcatcta	taacttatta	cagtcattcca	gccctgctgt	1080
aaaaatgaa	gctgctggga	cattagtgc	actctctagt	gcaccaactg	caatcaaggc	1140
tgctgctcag	tggtacattg	athtaattat	taaggagagc	gacaacaatg	taaaactcat	1200
agttttggat	cgcttgatag	aattaaaaga	gcctcctgct	catgaacgag	tactacagga	1260
tctgggttatg	gatatcctaa	gagtattgag	cacaccagac	ttagaagtac	gaaagaaaac	1320
tctgcagtta	gcactggatc	ttgtctcttc	tagaaatggt	gaagagctgg	ttattgtcct	1380
gaagaaggaa	gtgataaaaa	caaataatgt	gtctgagcat	gaagatactg	acaaatacag	1440
acaactccta	gtgcgaacat	tgcattctctg	ttctgtccga	ttccagata	tggtctgcaa	1500
tgttattcct	gtgttaattg	aatttctcag	tgacaacaac	gaagcagcag	ctgctgatgt	1560
cttgaggttt	gttcgtgaag	ccattcagcg	ctttgataac	ctgagaatgc	ttattgttga	1620
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aaaacctgaa	gaagaataaa	ctgtagggcc	agttcagaaa	ttggttactg	aaatgggtac	1860
ctatgcaact	cagagtgcct	ttagcagttc	tagaccacc	aagaaagagg	aagacagacc	1920
tcccttgaga	ggattccctc	tggtatggaga	ttctcttgg	gctgcctccc	ttgccacaac	1980
tctgaccaag	attgcattgc	gctatgtagc	tttggttcag	gagaagaaaa	agcaaaattc	2040
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tcctaagaag	ccaattactg	atgatgatgt	ggatcgaaat	tcctgtgccc	tcaaggctct	2160
gtctgaatgt	tcacctttaa	tgaatgacat	tttcaataag	gaatgcagac	agtccttttc	2220
tcacatgtta	tctgctaaac	tagaagaaga	gaaattatcc	caaaagaaag	aatctgaaaa	2280
gaggaatgtg	acagtacagc	ctgatgacct	catttccttc	atgcaactaa	ctgctaagaa	2340
tgaaatgaac	tgcaagggaag	atcagtttca	gctgagttta	ctggcagcaa	tggttaacac	2400
acagaggaaa	gaggcagcag	atcccctagc	atctaaactt	aacaagggtca	cccaattgac	2460
agggttctca	gatcctgtat	atgcagaagc	ttacgttcat	gtcaaccaat	atgatattgt	2520
cctggatgta	cttggtgtga	accaaaccag	tgatactttg	cagaattgca	cattagaact	2580
agctacacta	ggggatctga	aacttggtga	aaagcgtct	cctttgactc	ttgctcctca	2640
tgacttcgca	aatattaaag	ctaactgtca	agttagcatca	acagaaaatg	gaataatttt	2700
tggtaatata	gtttatgatg	tctctggagc	agcaagtgc	agaaattgtg	tggttctcag	2760
tgatattcac	atcgacatca	tggtactatat	ccagcctgca	acttgcaactg	atgcagaatt	2820
ccgtcagatg	tgggccgaat	ttgaatggga	aaacaaagtg	acagtttaaca	ccaacatggg	2880
tgattttaat	gactacttac	agcacatatt	aaagtcaacc	aatatgaaat	gctgactcc	2940
agaaaaggcc	ctttctgggt	actgtggctt	tatggcagcc	aaactttatg	ctcgttccat	3000
atthtgggtgaa	gatgcacttg	caaatgtcag	cattgagaag	ccaattcacc	agggaccaga	3060
tgctgctggt	accggccata	taagaattcg	tgcaaaagagc	caggggaatgg	ccttaagtct	3120
tggtgataaaa	atcaacttgt	cacagaagaa	aactagtata	taaaaataaa	caaaaagtcc	3180
ttgaagcttt	acagttaatt	taggtatggg	cttactggac	tccaacatct	tttgtactct	3240
ttcatgctta	tatagaatct	gagttcatgc	tgaatacttt	tcagccaata	atthtatagcc	3300
tttcccttaa	atcaagattg	agtthtaaat	tatagtttgt	cttttgtctt	aacagttctg	3360
aatgctgtcc	tcaaagtata	taatgtttca	tgtaccaaga	cccttttcac	agtacaataa	3420
acagatctat	tcataaaatt	ttgttatttt	ataaataaat	gattacataa	ttttagttat	3480
aaaaaaaaaa	aaaaaaaaaa	agaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		3528

<210> 20

<211> 953

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 20

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Met Thr Ala Ala Glu Asn Val Cys Tyr Thr Leu Ile Asn Val Pro Met
1      5      10      15
Asp Ser Glu Pro Ser Glu Ile Ser Leu Lys Asn Asp Leu Glu Lys
20      25      30
Gly Asp Val Lys Ser Lys Thr Glu Ala Leu Lys Lys Val Ile Ile Met
35      40      45
Ile Leu Asn Gly Glu Lys Leu Pro Gly Leu Leu Met Thr Ile Ile Arg
50      55      60
Phe Val Leu Pro Leu Gln Asp His Thr Ile Lys Lys Leu Leu Leu Val
65      70      75      80
Phe Trp Glu Ile Val Pro Lys Thr Thr Pro Asp Gly Arg Leu Leu His
85      90      95
Glu Met Ile Leu Val Cys Asp Ala Tyr Arg Lys Asp Leu Gln His Pro
100      105      110
Asn Glu Phe Ile Arg Gly Ser Thr Leu Arg Phe Leu Cys Lys Leu Lys
115      120      125
Glu Ala Glu Leu Leu Glu Pro Leu Met Pro Ala Ile Arg Ala Cys Leu
130      135      140
Glu His Arg His Ser Tyr Val Arg Arg Asn Ala Val Leu Ala Ile Tyr
145      150      155      160
Thr Ile Tyr Arg Asn Phe Glu His Leu Ile Pro Asp Ala Pro Glu Leu
165      170      175
Ile His Asp Phe Leu Val Asn Glu Lys Asp Ala Ser Cys Lys Arg Asn
180      185      190
Ala Phe Met Met Leu Ile His Ala Asp Gln Asp Arg Ala Leu Asp Tyr
195      200      205
Leu Ser Thr Cys Ile Asp Gln Val Gln Thr Phe Gly Asp Ile Leu Gln
210      215      220
Leu Val Ile Val Glu Leu Ile Tyr Lys Val Cys His Ala Asn Pro Ser
225      230      235      240
Glu Arg Ala Arg Phe Ile Arg Cys Ile Tyr Asn Leu Leu Gln Ser Ser
245      250      255
Ser Pro Ala Val Lys Tyr Glu Ala Ala Gly Thr Leu Val Thr Leu Ser
260      265      270
Ser Ala Pro Thr Ala Ile Lys Ala Ala Ala Gln Cys Tyr Ile Asp Leu
275      280      285
Ile Ile Lys Glu Ser Asp Asn Asn Val Lys Leu Ile Val Leu Asp Arg
290      295      300
Leu Ile Glu Leu Lys Glu His Pro Ala His Glu Arg Val Leu Gln Asp
305      310      315      320
Leu Val Met Asp Ile Leu Arg Val Leu Ser Thr Pro Asp Leu Glu Val
325      330      335
Arg Lys Lys Thr Leu Gln Leu Ala Leu Asp Leu Val Ser Ser Arg Asn
340      345      350
Val Glu Glu Leu Val Ile Val Leu Lys Lys Glu Val Ile Lys Thr Asn
355      360      365
Asn Val Ser Glu His Glu Asp Thr Asp Lys Tyr Arg Gln Leu Leu Val
370      375      380
Arg Thr Leu His Ser Cys Ser Val Arg Phe Pro Asp Met Ala Ala Asn
385      390      395      400
Val Ile Pro Val Leu Met Glu Phe Leu Ser Asp Asn Asn Glu Ala Ala
405      410      415
Ala Ala Asp Val Leu Glu Phe Val Arg Glu Ala Ile Gln Arg Phe Asp
420      425      430
Asn Leu Arg Met Leu Ile Val Glu Lys Met Leu Glu Val Phe His Ala
435      440      445

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Ile Lys Ser Val Lys Ile Tyr Arg Gly Ala Leu Trp Ile Leu Gly Glu
 450 455 460
 Tyr Cys Ser Thr Lys Glu Asp Ile Gln Ser Val Met Thr Glu Ile Arg
 465 470 475 480
 Arg Ser Leu Gly Glu Ile Pro Ile Val Glu Ser Glu Ile Lys Lys Glu
 485 490 495
 Ala Gly Glu Leu Lys Pro Glu Glu Glu Ile Thr Val Gly Pro Val Gln
 500 505 510
 Lys Leu Val Thr Glu Met Gly Thr Tyr Ala Thr Gln Ser Ala Leu Ser
 515 520 525
 Ser Ser Arg Pro Thr Lys Lys Glu Glu Asp Arg Pro Pro Leu Arg Gly
 530 535 540
 Phe Leu Leu Asp Gly Asp Phe Phe Val Ala Ala Ser Leu Ala Thr Thr
 545 550 555 560
 Leu Thr Lys Ile Ala Leu Arg Tyr Val Ala Leu Val Gln Glu Lys Lys
 565 570 575
 Lys Gln Asn Ser Phe Val Ala Glu Ala Met Leu Leu Met Ala Thr Ile
 580 585 590
 Leu His Leu Gly Lys Ser Ser Leu Pro Lys Lys Pro Ile Thr Asp Asp
 595 600 605
 Asp Val Asp Arg Ile Ser Leu Cys Leu Lys Val Leu Ser Glu Cys Ser
 610 615 620
 Pro Leu Met Asn Asp Ile Phe Asn Lys Glu Cys Arg Gln Ser Leu Ser
 625 630 635 640
 His Met Leu Ser Ala Lys Leu Glu Glu Glu Lys Leu Ser Gln Lys Lys
 645 650 655
 Glu Ser Glu Lys Arg Asn Val Thr Val Gln Pro Asp Asp Pro Ile Ser
 660 665 670
 Phe Met Gln Leu Thr Ala Lys Asn Glu Met Asn Cys Lys Glu Asp Gln
 675 680 685
 Phe Gln Leu Ser Leu Leu Ala Ala Met Gly Asn Thr Gln Arg Lys Glu
 690 695 700
 Ala Ala Asp Pro Leu Ala Ser Lys Leu Asn Lys Val Thr Gln Leu Thr
 705 710 715 720
 Gly Phe Ser Asp Pro Val Tyr Ala Glu Ala Tyr Val His Val Asn Gln
 725 730 735
 Tyr Asp Ile Val Leu Asp Val Leu Val Val Asn Gln Thr Ser Asp Thr
 740 745 750
 Leu Gln Asn Cys Thr Leu Glu Leu Ala Thr Leu Gly Asp Leu Lys Leu
 755 760 765
 Val Glu Lys Pro Ser Pro Leu Thr Leu Ala Pro His Asp Phe Ala Asn
 770 775 780
 Ile Lys Ala Asn Val Lys Val Ala Ser Thr Glu Asn Gly Ile Ile Phe
 785 790 795 800
 Gly Asn Ile Val Tyr Asp Val Ser Gly Ala Ala Ser Asp Arg Asn Cys
 805 810 815
 Val Val Leu Ser Asp Ile His Ile Asp Ile Met Asp Tyr Ile Gln Pro
 820 825 830
 Ala Thr Cys Thr Asp Ala Glu Phe Arg Gln Met Trp Ala Glu Phe Glu
 835 840 845
 Trp Glu Asn Lys Val Thr Val Asn Thr Asn Met Val Asp Leu Asn Asp
 850 855 860
 Tyr Leu Gln His Ile Leu Lys Ser Thr Asn Met Lys Cys Leu Thr Pro
 865 870 875 880
 Glu Lys Ala Leu Ser Gly Tyr Cys Gly Phe Met Ala Ala Asn Leu Tyr
 885 890 895
 Ala Arg Ser Ile Phe Gly Glu Asp Ala Leu Ala Asn Val Ser Ile Glu
 900 905 910
 Lys Pro Ile His Gln Gly Pro Asp Ala Ala Val Thr Gly His Ile Arg
 915 920 925

Ile Arg Ala Lys Ser Gln Gly Met Ala Leu Ser Leu Gly Asp Lys Ile
 930 935 940
 Asn Leu Ser Gln Lys Lys Thr Ser Ile
 945 950

<210> 21
 <211> 3075
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 21
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 cccaccgact ccactatggt gaagaaattc gacaagaagg atgaggagtc aggtggaggc 120
 tccaacccat tccagcacct tgagaagagt gcggtactcc aggaggcccg tgtatttaat 180
 gaaactccca tcaaccctcg gaaatgtgcc cacatcctca ccaagattct ttatctcata 240
 aaccaggggg agcacctggg gaccacggaa gcgaccgagg ccttctttgc catgaccaag 300
 ctctttcagt ccaatgacct cacactccgt cggatgtgct acttgacct caaggagatg 360
 tcttgcatgg cagaggatgt catcattgtc accagcagcc taacaaaaga catgactggg 420
 aaagaagaca actaccgggg cccggccgtg cgagccctct gccagatcac tgatagcacc 480
 atgctgcagg ctattgagcg ctacatgaaa caagccattg tggacaagggt gccagtgctc 540
 tccagctctg ccctcgtgtc ttccttgca cctgtgaagt gcagctttga cgtgggtcaag 600
 cgctgggtga atgaggctca ggaggcagca tccagtata acatcatggt ccagtaccac 660
 gcactagggc tctgtacca tgtgcgtaag aatgaccgcc tagccgtcaa taagatgatc 720
 agcaaggcca caccgcatgg ccttaagtct ccctttgcct actgcatgat gatccgggtg 780
 gccagcaagc agctggaaga ggaggatggc agcgtgaca gccactggt tgacttcac 840
 gagagctgct tgcgcaacaa gcacgagatg gtggtgatg aagccgcctc ggccattgctc 900
 aacctgcctg ggtgcagcgc caaggagctg gccccagctg tctcagtgt ccagctcttc 960
 tgcagctccc ccaaggccgc cctccgttac gccgcgtcc gcacctcaa caagggtggc 1020
 atgaagcacc cgtccgctgt gacagcttgt aatctggatc tggagaacct ggtcacagat 1080
 tcaaaccgca gcattgccac gctggccatc accaccctcc ttaagacggg cagcgagagc 1140
 agcatcgacc gctcatgaa gcagatctcc tcttcatgt cagaatctc ggatgaattc 1200
 aagggtggtg ttgtccagcc catcagtgc cgggaagagg gtggtttga gtataagcgc 1260
 gtccttatga acttctgtt caccatgctg cgggaagagg gtggtttga gtataagcgc 1320
 gctatcgtgg actgcatcat cagcatcatt gaagagaact cagagagcaa ggagacaggg 1380
 ctgtcacatc tgtgcgagtt catcgaggac tgcgagttca cagtgtgtgc caccgtatt 1440
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 atctataacc gagtggctct ggagcatgag gaggtccggg cagggtgctgt gagtgtctc 1560
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 gagcagaagc agaaggccct taatgcaggc tatatcctaa atggtctgac tgtgtccatc 1740
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 ctcaagtctg tgcctctggc caccggcggc atggcagagc agagaacaga aagtacccc 1860
 atcacagcag tcaaacagcc tgagaaaagt gcagctacca ggcaggagat cttccaggag 1920
 cagttggcag cagtgcaga gttccgcggt cttgggcccc tcttcaagtc ctgcctgag 1980
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 aatgtcacag tgcagatgga gccactgag gcctatgagg tgctctgtta cgtgcctgcc 2160
 cggagcctgc cctacaacca gccggggacc tgctacacac tgggtggcact gcccaaagaa 2220
 gacccacagc ctgtggcctg cacttcagc tgcatgatga agttcactgt caaggactgt 2280
 gatccacca ctggggagac tgatgacgaa ggctatgagg atgagatgt gctggaagat 2340
 ctggaagtta ctgtagctga tcacattcaa aaggtcatga aactgaactt cgaagcagcc 2400
 tgggatgagg taggggatga atttgagaag gaggaacgt tcacctgtc taccatcaag 2460
 acacttgaag aggtgtggg taatattgtg aagttcttgg gaatgaccc ttgtgagagg 2520
 tcagacaaag tgcgggataa caagaacacc cacagcttgc tctggctgg tgtgtccgg 2580
 ggtggtcatg acatcctggg gcgctccgg ctgctgcttt tggacacagt gacaatgcag 2640
 gtgacagcca gaagtgtgga ggagctgcca gtagacatca tcttgcatc tgtgggataa 2700
 gaggccagcc tgcataggac ctcatacct tcccaacac tacctggaag ttgtgccttc 2760

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ctcatgaaac tggcagaaac cccttcccaa gcttctgtat tgaaaaacaa ttaggaatca 2820
ttgcagattt ttttttattc tgctcccacc tcccaccgg gactacttgc tggtgacttt 2880
tttttttttt ttttttaaat aggggatgat tttagcttgt cctaaatctt gctgtccacc 2940
cttccaggaa agggacattg taaatgaata aaacattctc aactcctctt gaatctatcc 3000
cccaagaaac catcttatcc ctgtaataaa tcagcatgta tttattgaaa aaaaaaaaaa 3060
aaaaaaaaaa aaaaaa 3075

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<210> 22

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

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Met Leu Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Gly Gly Ser
 1          5          10          15
Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
 20          25          30
Val Phe Asn Glu Thr Pro Ile Asn Pro Arg Lys Cys Ala His Ile Leu
 35          40          45
Thr Lys Ile Leu Tyr Leu Ile Asn Gln Gly Glu His Leu Gly Thr Thr
 50          55          60
Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Lys Leu Phe Gln Ser Asn
 65          70          75          80
Asp Pro Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ser
 85          90          95
Cys Ile Ala Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100          105          110
Met Thr Gly Lys Glu Asp Asn Tyr Arg Gly Pro Ala Val Arg Ala Leu
115          120          125
Cys Gln Ile Thr Asp Ser Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130          135          140
Lys Gln Ala Ile Val Asp Lys Val Pro Ser Val Ser Ser Ser Ala Leu
145          150          155          160
Val Ser Ser Leu His Leu Leu Lys Cys Ser Phe Asp Val Val Lys Arg
165          170          175
Trp Val Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180          185          190
Gln Tyr His Ala Leu Gly Leu Leu Tyr His Val Arg Lys Asn Asp Arg
195          200          205
Leu Ala Val Asn Lys Met Ile Ser Lys Val Thr Arg His Gly Leu Lys
210          215          220
Ser Pro Phe Ala Tyr Cys Met Met Ile Arg Val Ala Ser Lys Gln Leu
225          230          235          240
Glu Glu Glu Asp Gly Ser Arg Asp Ser Pro Leu Phe Asp Phe Ile Glu
245          250          255
Ser Cys Leu Arg Asn Lys His Glu Met Val Val Tyr Glu Ala Ala Ser
260          265          270
Ala Ile Val Asn Leu Pro Gly Cys Ser Ala Lys Glu Leu Ala Pro Ala
275          280          285
Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Ala Ala Leu Arg
290          295          300
Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305          310          315          320
Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Val Thr Asp Ser
325          330          335
Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly
340          345          350

```

Ser Glu Ser Ser Ile Asp Arg Leu Met Lys Gln Ile Ser Ser Phe Met
 355 360 365
 Ser Glu Ile Ser Asp Glu Phe Lys Val Val Val Gln Ala Ile Ser
 370 375 380
 Ala Leu Cys Gln Lys Tyr Pro Arg Lys His Ala Val Leu Met Asn Phe
 385 390 395 400
 Leu Phe Thr Met Leu Arg Glu Glu Gly Gly Phe Glu Tyr Lys Arg Ala
 405 410 415
 Ile Val Asp Cys Ile Ile Ser Ile Ile Glu Glu Asn Ser Glu Ser Lys
 420 425 430
 Glu Thr Gly Leu Ser His Leu Cys Glu Phe Ile Glu Asp Cys Glu Phe
 435 440 445
 Thr Val Leu Ala Thr Arg Ile Leu His Leu Leu Gly Gln Glu Gly Pro
 450 455 460
 Lys Thr Thr Asn Pro Ser Lys Tyr Ile Arg Phe Ile Tyr Asn Arg Val
 465 470 475 480
 Val Leu Glu His Glu Glu Val Arg Ala Gly Ala Val Ser Ala Leu Ala
 485 490 495
 Lys Phe Gly Ala Gln Asn Glu Glu Met Leu Pro Ser Ile Leu Val Leu
 500 505 510
 Leu Lys Arg Cys Val Met Asp Asp Asn Glu Val Arg Asp Arg Ala
 515 520 525
 Thr Phe Tyr Leu Asn Val Leu Glu Gln Lys Gln Lys Ala Leu Asn Ala
 530 535 540
 Gly Tyr Ile Leu Asn Gly Leu Thr Val Ser Ile Pro Gly Leu Glu Arg
 545 550 555 560
 Ala Leu Gln Gln Tyr Thr Leu Glu Pro Ser Glu Lys Pro Phe Asp Leu
 565 570 575
 Lys Ser Val Pro Leu Ala Thr Ala Pro Met Ala Glu Gln Arg Thr Glu
 580 585 590
 Ser Thr Pro Ile Thr Ala Val Lys Gln Pro Glu Lys Val Ala Ala Thr
 595 600 605
 Arg Gln Glu Ile Phe Gln Glu Gln Leu Ala Ala Val Pro Glu Phe Arg
 610 615 620
 Gly Leu Gly Pro Leu Phe Lys Ser Ser Pro Glu Pro Val Ala Leu Thr
 625 630 635 640
 Glu Ser Glu Thr Glu Tyr Val Ile Arg Cys Thr Lys His Thr Phe Thr
 645 650 655
 Asn His Met Val Phe Gln Phe Asp Cys Thr Asn Thr Leu Asn Asp Gln
 660 665 670
 Thr Leu Glu Asn Val Thr Val Gln Met Glu Pro Thr Glu Ala Tyr Glu
 675 680 685
 Val Leu Cys Tyr Val Pro Ala Arg Ser Leu Pro Tyr Asn Gln Pro Gly
 690 695 700
 Thr Cys Tyr Thr Leu Val Ala Leu Pro Lys Glu Asp Pro Thr Ala Val
 705 710 715 720
 Ala Cys Thr Phe Ser Cys Met Met Lys Phe Thr Val Lys Asp Cys Asp
 725 730 735
 Pro Thr Thr Gly Glu Thr Asp Asp Glu Gly Tyr Glu Asp Glu Tyr Val
 740 745 750
 Leu Glu Asp Leu Glu Val Thr Val Ala Asp His Ile Gln Lys Val Met
 755 760 765
 Lys Leu Asn Phe Glu Ala Ala Trp Asp Glu Val Gly Asp Glu Phe Glu
 770 775 780
 Lys Glu Glu Thr Phe Thr Leu Ser Thr Ile Lys Thr Leu Glu Glu Ala
 785 790 795 800
 Val Gly Asn Ile Val Lys Phe Leu Gly Met His Pro Cys Glu Arg Ser
 805 810 815
 Asp Lys Val Pro Asp Asn Lys Asn Thr His Thr Leu Leu Leu Ala Gly
 820 825 830

[illegible]

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<210> 23
<211> 3110
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 23									
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atgattaaaa	aattcgacaa	gaaggacgag	gagtcctgta	gtggctccaa	tcctttccag				120
catctggaga	agagtctcgt	tttcacaggag	gtctcgtatat	tcfaatgaac	tcfaatcaat				180
ccaagaagat	gtttgcata	tcttcaaaa	atctcttact	tactgaacca	gggtgaacac				240
tttggaaaca	cggaagctac	agaagccttc	tttgcaatga	cgcgattgtt	tcfaatcta				300
gatcaaacat	tgaggagaat	gtgtcacctt	accatcaaag	aatgggttac	catctctgag				360
gatgtgataa	ttgtcacaga	cagctctgact	aaagacatga	ctggaaaaga	agatgtatac				420
cgaggtccgg	ccatcagagc	tctctgcagg	atcacccgat	gaacaatgtt	gcaagccatt				480
gaaagataca	tgaagcaggc	catttgggat	aaagtttcca	gtgtattccag	ttcagcactg				540
gtatcttccc	tgacatgat	gaagataagc	tatgatgtgg	ttaagcgctg	gatcaatgaa				600
gcccagaaga	ctgcataca	tgataatatt	atggtccagt	accatgcatt	gggagtcctg				660
tatcacctta	gaaagaatga	tcgactttgt	gtttccaaga	tgttgaataa	gtttactaaa				720
tctgggtctca	agtcacagtc	tgtcttactgc	atgtctatcc	gaattggccag	tcgcttacta				780
aaagaaactg	aggatggcca	tgaagtgcca	ctgtttgatt	tcattgagag	ctgcttgcca				840
aataaacatg	aatgtggtat	ttatgaagct	gcttcagcta	tcattccatt	tcctaactgc				900
actgcaagag	agttggcacc	tgtcttttca	gtttctcaac	ttttctgtag	ttctctcaag				960
ccagctctga	gatatgcagc	tgttgaggacc	ttgaacaagg	tggcaattgaa	gcaccctctt				1020
gctgttactg	cctgcaatct	ggacttagaa	aacttaatac	cagactcaaa	cagaagcatt				1080
gctaccttag	ccattactac	actcctcaaa	acaggaagtg	agagcagtg	ggaccggctc				1140
atgaagcaga	tatcttcttt	tgtgtctgaa	atctcagatg	agttcaaggt	gggtggtgta				1200
caggcaatta	gtgctctctg	tcagaataac	cctcgaaagc	acaggttcac	gatgactttc				1260
ctctccaaca	tgctccgaga	tgatggaggc	tttgatgaca	agcgtgcatt	tgtggactgt				1320
ataatcagca	ttgtggaaga	gaaccctgag	agtaaagaag	caggccctagc	ccacctttgt				1380
gaattcattg	aggactgtga	acacactgtt	ctggctacta	agattctaca	cttgttgggc				1440
aaagagggcc	ctagaagcgc	tgtcccctcc	aaatatatcc	gttttatttt	taatagggtt				1500
gtcctggaga	atgagctgtg	cagagctgct	gctgtgagtg	ctttggctaa	tttggggct				1560
cagaatgaga	gtcttctccc	aagcatcctt	gtactcttac	agaggtgtat	gatggactact				1620
gatgacgggg	tacgagacag	agctaccttc	tatctgaatg	tgctgcagca	gaggcagatg				1680
gcactaaagt	ccacatata	ctttaatggt	ttgacggctt	ctgtaccagg	gatggaaaaa				1740
gcttaccacc	agtcacagtt	ggagccttca	gaaaaaccgt	ttgacatgaa	atcaattctt				1800
cttgctatgg	ctcctgtctt	tgaacagaaa	gcagaaatca	cacttgtggc	tactaagcca				1860
gagaagttgg	ctccttccag	gcaagacatt	ttccaagaac	aattggctgc	cattcctgag				1920
tttttgataa	taggaccctt	gttcaagctt	tctgagcctg	ttcaacttac	agaagcagag				1980
acagaatatt	ttgttcgatg	tatcaagcac	atgtttacca	atcacatcgt	gttccagttt				2040
gactgcacca	acacttccaa	tgaccagctg	ctggaaaaag	tcagactgca	gatggagcca				2100
tcagatttct	atgaagtgtc	gtcttgtatc	ccagccccc	gccttcccta	taaccaacca				2160
ggaatatggt	acactcttgt	tcgtttgcct	gatgatgacc	ctacagcagt	tgcaaggctcc				2220
tttagctgca	ccatgaagtt	tacagtcagg	gactgtgacc	ctaacactgg	agttccagat				2280
gaggatgggt	atgatgatga	gtatgtgctg	gaagatctcg	aagtgaactg	gtctgaccat				2340
attcagaaaag	tactgaagcc	taactttgct	gctgcttggg	aagaggtggg	agataccttt				2400
gagaaagagg	aaacctttgc	cctcagctct	accaaaacc	ttgaagaggc	tgtcaacaat				2460
atcatcacat	ttctgggcat	gcagccatgt	gagaggtccg	ataaagtacc	tgagaaacaag				2520
aattcccaat	cgtcttatct	ggcaggtata	ttcagaggtg	gctatgattt	attggtgagg				2580
tccaggctgg	ccttagccga	tggagtgacc	atgcagggtg	ctgtcgaag	taaagagaga				2640

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acacctgtag atgttatctt agcttctgtt ggataaatgc ttactggaca agaggaaact 2700
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cttttgaaga tgaatgactt tggagaagca aattaaacat ttggccctga gccagcagat 2820
caagcaaatg tctatctttg cgcattgggtt gttttttttt tttttctttt tattctactt 2880
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tggaaaattt ttatcccaga ggggtggggg ggagggggga ggggaagcca gagtccactt 3060
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<210> 24

<211> 871

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 24

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Met Ile Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Ser Gly Ser
1           5           10          15
Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
20          25          30
Ile Phe Asn Glu Thr Pro Ile Asn Pro Arg Arg Cys Leu His Ile Leu
35          40          45
Thr Lys Ile Leu Tyr Leu Leu Asn Gln Gly Glu His Phe Gly Thr Thr
50          55          60
Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Arg Leu Phe Gln Ser Asn
65          70          75          80
Asp Gln Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ala
85          90          95
Thr Ile Ser Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100         105         110
Met Thr Gly Lys Glu Asp Val Tyr Arg Gly Pro Ala Ile Arg Ala Leu
115         120         125
Cys Arg Ile Thr Asp Gly Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130         135         140
Lys Gln Ala Ile Val Asp Lys Val Ser Ser Val Ser Ser Ala Leu
145         150         155         160
Val Ser Ser Leu His Met Met Lys Ile Ser Tyr Asp Val Val Lys Arg
165         170         175
Trp Ile Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180         185         190
Gln Tyr His Ala Leu Gly Val Leu Tyr His Leu Arg Lys Asn Asp Arg
195         200         205
Leu Ala Val Ser Lys Met Leu Asn Lys Phe Thr Lys Ser Gly Leu Lys
210         215         220
Ser Gln Phe Ala Tyr Cys Met Leu Ile Arg Ile Ala Ser Arg Leu Leu
225         230         235         240
Lys Glu Thr Glu Asp Gly His Glu Ser Pro Leu Phe Asp Phe Ile Glu
245         250         255
Ser Cys Leu Arg Asn Lys His Glu Met Val Ile Tyr Glu Ala Ala Ser
260         265         270
Ala Ile Ile His Leu Pro Asn Cys Thr Ala Arg Glu Leu Ala Pro Ala
275         280         285
Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Pro Ala Leu Arg
290         295         300
Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305         310         315         320
Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Ile Thr Asp Ser
325         330         335

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Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly
 340 345 350
 Ser Glu Ser Ser Val Asp Arg Leu Met Lys Gln Ile Ser Ser Phe Val
 355 360 365
 Ser Glu Ile Ser Asp Glu Phe Lys Val Val Val Val Gln Ala Ile Ser
 370 375 380
 Ala Leu Cys Gln Lys Tyr Pro Arg Lys His Ser Val Met Met Thr Phe
 385 390 395 400
 Leu Ser Asn Met Leu Arg Asp Asp Gly Gly Phe Glu Tyr Lys Arg Ala
 405 410 415
 Ile Val Asp Cys Ile Ile Ser Ile Val Glu Glu Asn Pro Glu Ser Lys
 420 425 430
 Glu Ala Gly Leu Ala His Leu Cys Glu Phe Ile Glu Asp Cys Glu His
 435 440 445
 Thr Val Leu Ala Thr Lys Ile Leu His Leu Leu Gly Lys Glu Gly Pro
 450 455 460
 Arg Thr Pro Val Pro Ser Lys Tyr Ile Arg Phe Ile Phe Asn Arg Val
 465 470 475 480
 Val Leu Glu Asn Glu Ala Val Arg Ala Ala Val Ser Ala Leu Ala
 485 490 495
 Lys Phe Gly Ala Gln Asn Glu Ser Leu Leu Pro Ser Ile Leu Val Leu
 500 505 510
 Leu Gln Arg Cys Met Met Asp Thr Asp Asp Glu Val Arg Asp Arg Ala
 515 520 525
 Thr Phe Tyr Leu Asn Val Leu Gln Gln Arg Gln Met Ala Leu Asn Ala
 530 535 540
 Thr Tyr Ile Phe Asn Gly Leu Thr Val Ser Val Pro Gly Met Glu Lys
 545 550 555 560
 Ala Leu His Gln Tyr Thr Leu Glu Pro Ser Glu Lys Pro Phe Asp Met
 565 570 575
 Lys Ser Ile Pro Leu Ala Met Ala Pro Val Phe Glu Gln Lys Ala Glu
 580 585 590
 Ile Thr Leu Val Ala Thr Lys Pro Glu Lys Leu Ala Pro Ser Arg Gln
 595 600 605
 Asp Ile Phe Gln Glu Gln Leu Ala Ala Ile Pro Glu Phe Leu Asn Ile
 610 615 620
 Gly Pro Leu Phe Lys Ser Ser Glu Pro Val Gln Leu Thr Glu Ala Glu
 625 630 635 640
 Thr Glu Tyr Phe Val Arg Cys Ile Lys His Met Phe Thr Asn His Ile
 645 650 655
 Val Phe Gln Phe Asp Cys Thr Asn Thr Leu Asn Asp Gln Leu Leu Glu
 660 665 670
 Lys Val Thr Val Gln Met Glu Pro Ser Asp Ser Tyr Glu Val Leu Ser
 675 680 685
 Cys Ile Pro Ala Pro Ser Leu Pro Tyr Asn Gln Pro Gly Ile Cys Tyr
 690 695 700
 Thr Leu Val Arg Leu Pro Asp Asp Asp Pro Thr Ala Val Ala Gly Ser
 705 710 715 720
 Phe Ser Cys Thr Met Lys Phe Thr Val Arg Asp Cys Asp Pro Asn Thr
 725 730 735
 Gly Val Pro Asp Glu Asp Gly Tyr Asp Asp Glu Tyr Val Leu Glu Asp
 740 745 750
 Leu Glu Val Thr Val Ser Asp His Ile Gln Lys Val Leu Lys Pro Asn
 755 760 765
 Phe Ala Ala Ala Trp Glu Glu Val Gly Asp Thr Phe Glu Lys Glu Glu
 770 775 780
 Thr Phe Ala Leu Ser Ser Thr Lys Thr Leu Glu Glu Ala Val Asn Asn
 785 790 795 800
 Ile Ile Thr Phe Leu Gly Met Gln Pro Cys Glu Arg Ser Asp Lys Val
 805 810 815

Pro Glu Asn Lys Asn Ser His Ser Leu Tyr Leu Ala Gly Ile Phe Arg
 820 825 830
 Gly Gly Tyr Asp Leu Leu Val Arg Ser Arg Leu Ala Leu Ala Asp Gly
 835 840 845
 Val Thr Met Gln Val Thr Val Arg Ser Lys Glu Arg Thr Pro Val Asp
 850 855 860
 Val Ile Leu Ala Ser Val Gly
 865 870

<210> 25

<211> 1900

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 25

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ttccctgtat	actgtcaaa	ccatcctgat	tctggacaat	gatggagatc	gactttttgc	120
caagtactat	gacgacacct	acccagtggt	caaggagcaa	aaggcctttg	agaagaacat	180
tttcaacaag	acccatcgga	ctgacagtga	aattgccctc	ttggaaggcc	tgacagtggg	240
atacaaaagc	agtatagatc	tctatttcta	tgtgattggc	agctcctatg	aaaatgagct	300
gatgcttatg	gctgttctga	actgtctctt	cgactcattg	agccagatgc	tgaggaaaaa	360
tgtagaaaa	cgagcactgc	tggagaacat	ggaggggctg	ttcttggctg	tggatgaaat	420
tgtagatgga	ggggtgatcc	tagagagtga	tcccagcag	gtggtacacc	gggtggcatt	480
aaggggtgaa	gatgtcccc	ttacggagca	gaccgtgtct	caggtgctgc	agtcagccaa	540
agaacagatc	aagtggtcac	tccttcgggtg	aagacctcac	tgttcctggc	tcttcacctc	600
cttcaaaaaa	tttgcattgc	tgctgtgaat	tttcatctag	ttccccaatc	gatgctctca	660
gggtcatctc	ggggatcaca	gggatcctta	aatctccatt	ctgtttgtgg	ttgccccctc	720
aacctcccct	acacccttcc	tattcttttt	cattcttctt	gcagttctgg	gagtaaagct	780
cccagcatat	ttagataata	gggcagggga	agcaccctct	ttctttctag	actggattat	840
gctcacatgc	tcccttgccc	tgacattttt	gtaaattctg	tgccctttgc	tgtagctaca	900
cttcagatta	aagtaggaga	aagaatgtgc	tgagtgtttt	cctccctttg	cctctacctg	960
gccctcatcc	caacagccca	gcaaggggag	agagaaaagag	aattcttttc	tatagaacga	1020
gtgggggctg	ggatgggtag	ggatttatcc	aatctaagcc	ctaaccctac	ttagtgcact	1080
cagtgttttc	ttccattcct	tcttactgcc	ctgtcctctg	ccttgggaaga	ggctttggga	1140
atagttcata	gggaaggagc	aacatggaag	aaacagcgat	ttaaattgta	ttgaacaggg	1200
catataaaat	gcattctgta	ccctgatctg	gcataatagc	tcaaaaactgc	agtggcgagt	1260
gtccatctct	tagttagcta	ccttaactgt	ccacccttac	tacctgtggg	atcgttgcct	1320
ggtttgtctt	ctctgtgtcc	tggagcaaa	ccagttccta	aaactaaaac	tccattctag	1380
tcttgggaag	aaaagtttct	actcagaact	ggggaaggag	tggaaacttat	gacttgggcc	1440
tctaggctgt	ctctgtcccc	tcagctcccc	gacatgcatt	tactctctgc	cgtgggtctg	1500
cagtcgctgc	aacctaccct	ctctctgcct	cagccttaca	cccaagcagt	aggtctgtgc	1560
tctccctgtc	tctaggtcgc	tgagagaggt	gcttttcttc	ataaaaactt	tgggggtttg	1620
atttccccag	gaagatggag	aatggaatac	tcactcttgg	gtctaactct	tccccctgac	1680
ccagaacttc	ctccccacaa	aaatgccttt	aaaaaccttc	ctgagactta	agcattctgc	1740
cccacttact	aactgccagt	tctccagcac	tgaggtgggg	cagataacgg	ggcatattta	1800
agggggcatc	tttgtgtaaa	agatgcatgg	agtcaggaga	aaaccacctt	cataaactgc	1860
tctgtgcaaa	gaggaataaa	acattttttc	caaactgaaa			1900

<210> 26

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 26
 Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile
 1 5 10 15
 Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp
 20 25 30
 Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile
 35 40 45
 Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly
 50 55 60
 Leu Thr Val Val Tyr Lys Ser Ser Ile Asp Leu Tyr Phe Tyr Val Ile
 65 70 75 80
 Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ala Val Leu Asn Cys
 85 90 95
 Leu Phe Asp Ser Leu Ser Gln Met Leu Arg Lys Asn Val Glu Lys Arg
 100 105 110
 Ala Leu Leu Glu Asn Met Glu Gly Leu Phe Leu Ala Val Asp Glu Ile
 115 120 125
 Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Val His
 130 135 140
 Arg Val Ala Leu Arg Gly Glu Asp Val Pro Leu Thr Glu Gln Thr Val
 145 150 155 160
 Ser Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu Leu
 165 170 175
 Arg

<210> 27
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 27
 Cys Glu Ser Gly Glu Leu Lys Pro Glu Asp Asp Val Thr Val Gly Pro
 1 5 10 15
 Ala Gln Lys

<210> 28
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 28
 Gly Asn Met Phe Ala Asn Leu Phe Lys Gly Leu Phe Gly Lys Lys Glu
 1 5 10 15

<210> 29
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =

synthetic construct

<400> 29

Glu Lys Lys Gly Phe Leu Gly Lys Phe Leu Asn Ala Phe Met Asn Gly
1 5 10 15

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 30

Cys Thr His Pro Phe Thr His Glu Cys Gly Gly Gly Ser
1 5 10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 31

Cys Gly Glu His Val Arg Pro Ser Cys Gly Gly Gly Ser
1 5 10

<210> 32

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 32

Cys Asn Asn Thr Arg Ser Pro Tyr Cys Gly Gly Gly Ser
1 5 10

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 33

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<210> 34
 <211> 3916
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 34
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<210> 35

<211> 511

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 35

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Leu Ala Ala Phe Pro Lys Leu Met Asn Thr Gly Lys Gln His Thr Phe
35     40     45
Val Glu Thr Glu Ser Val Arg Tyr Val Tyr Gln Pro Met Glu Lys Leu
50     55     60
Tyr Met Val Leu Ile Thr Thr Lys Asn Ser Asn Ile Leu Glu Asp Leu
65     70     75     80
Glu Thr Leu Arg Leu Phe Ser Arg Val Ile Pro Glu Tyr Cys Arg Ala
85     90     95
Leu Glu Glu Asn Glu Ile Ser Glu His Cys Phe Asp Leu Ile Phe Ala
100    105    110
Phe Asp Glu Ile Val Ala Leu Gly Tyr Arg Glu Asn Val Asn Leu Ala
115    120    125
Gln Ile Arg Thr Phe Thr Glu Met Asp Ser His Glu Glu Lys Val Phe
130    135    140
Arg Ala Val Arg Glu Thr Gln Glu Arg Glu Ala Lys Ala Glu Met Arg
145    150    155    160
Arg Lys Ala Lys Glu Leu Gln Gln Ala Arg Arg Asp Ala Glu Arg Gln
165    170    175
Gly Lys Lys Ala Pro Gly Phe Gly Gly Phe Gly Ser Ser Ala Val Ser
180    185    190
Gly Gly Ser Thr Ala Ala Met Ile Thr Glu Thr Ile Ile Glu Thr Asp
195    200    205
Lys Pro Lys Val Ala Pro Ala Pro Ala Arg Pro Ser Gly Pro Ser Lys
210    215    220
Ala Leu Lys Leu Gly Ala Lys Gly Lys Glu Val Asp Asn Phe Val Asp
225    230    235    240
Lys Leu Lys Ser Glu Gly Glu Thr Ile Met Ser Ser Ser Met Gly Lys
245    250    255
Arg Thr Ser Glu Ala Thr Lys Met His Ala Pro Pro Ile Asn Met Glu
260    265    270

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Ser Val His Met Lys Ile Glu Glu Lys Ile Thr Leu Thr Cys Gly Arg
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 Asp Gly Gly Leu Gln Asn Met Glu Leu His Gly Met Ile Met Leu Arg
 290 295 300
 Ile Ser Asp Asp Lys Tyr Gly Arg Ile Arg Leu His Val Glu Asn Glu
 305 310 315 320
 Asp Lys Lys Gly Val Gln Leu Gln Thr His Pro Asn Val Asp Lys Lys
 325 330 335
 Leu Phe Thr Ala Glu Ser Leu Ile Gly Leu Lys Asn Pro Glu Lys Ser
 340 345 350
 Phe Pro Val Asn Ser Asp Val Gly Val Leu Lys Trp Arg Leu Gln Thr
 355 360 365
 Thr Glu Glu Ser Phe Ile Pro Leu Thr Ile Asn Cys Trp Pro Ser Glu
 370 375 380
 Ser Gly Asn Gly Cys Asp Val Asn Ile Glu Tyr Glu Leu Gln Glu Asp
 385 390 395 400
 Asn Leu Glu Leu Asn Asp Val Val Ile Thr Ile Pro Leu Pro Ser Gly
 405 410 415
 Val Gly Ala Pro Val Ile Gly Glu Ile Asp Gly Glu Tyr Arg His Asp
 420 425 430
 Ser Arg Arg Asn Thr Leu Glu Trp Cys Leu Pro Val Ile Asp Ala Lys
 435 440 445
 Asn Lys Ser Gly Ser Leu Glu Phe Ser Ile Ala Gly Gln Pro Asn Asp
 450 455 460
 Phe Phe Pro Val Gln Val Ser Phe Val Ser Lys Lys Asn Tyr Cys Asn
 465 470 475 480
 Ile Gln Val Thr Lys Val Thr Gln Val Asp Gly Asn Ser Pro Val Arg
 485 490 495
 Phe Ser Thr Glu Thr Thr Phe Leu Val Asp Lys Tyr Glu Ile Leu
 500 505 510